

SEQUENCE LISTING

<110> Genencor International, Inc.
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<120> Serine Proteases, Nucleic Acids Encoding Serine Enzymes and
Vectors and Host Cells Incorporating Same

<130> GC819-2-US/B

<140> 10/576,331

<141> 2006-04-18

<150> US 60/523,609

<151> 2003-11-19

<160> 656

<170> PatentIn version 3.2

<210> 1

<211> 1680

<212> DNA

<213> Cellulomonas strain 69B4

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<212> DNA

<213> Cellulomonas strain 69B4

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<213> Cellulomonas spp.

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 <213> Cellulomonas strain 69B4

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Val	Val	Ala	Val	Lys	Ala	Gly	Ala	Gln	Asp	Val	Ala	Ala	Gly	Leu	Val		
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Pro	Thr	Gly	Thr	Phe	Ala	Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala		
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Tyr	Ser	Gly	Gly	Arg	Val	Gln	Val	Ala	Gly	His	Thr	Ala	Ala	Pro	Val		
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Arg	Gly	Leu	Ile	Arg	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly		
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Phe	Thr	Gly	Thr	Leu	Ala	Ala	Gly	Arg	Ala	Ala	Ala	Gln	Pro	Asn	Gly		
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 <212> PRT

<213> Cellulomonas strain 69B4

<400> 7

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 <213> Cellulomonas spp.

<400> 8

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Gln	Val	Ala	Gly	His	Thr	Ala	Ala	Pro	Val	Gly	Ser	Ala	Val	Cys	Arg		
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<400> 12

Asp	Gly	Trp	Asp	Cys	Gly	Thr	Ile	Thr	Ala	Leu	Asn	Ser	Ser	Val	Thr
1				5					10					15	
Tyr	Pro	Glu	Gly	Thr	Val	Arg	Gly	Leu	Ile	Arg	Thr	Thr	Val	Cys	Ala
			20					25					30		
Glu	Pro	Gly	Asp	Ser	Gly	Gly	Ser	Leu	Leu	Ala	Gly	Asn	Gln	Ala	Gln
		35					40					45			
Gly	Val	Thr	Ser	Gly	Asp	Ser	Gly	Gly	Ser						

50

55

<210> 13
 <211> 177
 <212> DNA
 <213> Cellulomonas strain 69B4

acgacgggctg	ggactgcggc	accatcactg	cgctcaactc	ctcggtcacc	taccccgagg	60
gcaccgtccg	cggcctgac	cgcaccaccg	tctgcgccga	gcccggcgac	tccggtggct	120
cgctgctcgc	cggcaaccag	gcccagggcg	tcacgtccgg	cgactccggc	ggctcat	177

<210> 14
 <211> 32

<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 14
cggggtaggt gaccgaggag ttgagcgag tg

32

<210> 15
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 15
gctcgccggc aaccaggccc agggcgtcac gtc

33

<210> 16
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 16
aacggcgggt tcataccgc cggccactgc ggcc

34

<210> 17
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> N-terminus of the mature chain determined by MALDI-TOF analysis

<400> 17

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg
1 5 10

<210> 18
<211> 189
<212> PRT
<213> Cellulomonas strain 69B4

<400> 18

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg
1 5 10 15
Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His
20 25 30
Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala

<400> 20

Ile Ala Gly Gly Glu Ala Ile Tyr Ala Ala Gly Gly Gly Arg Cys Ser
1 5 10 15
Leu Gly Phe Asn Val Arg Ser Ser Ser Gly Ala Thr Tyr Ala Leu Thr
20 25 30
Ala Gly His Cys Thr Glu Ile Ala Ser Thr Trp Tyr Thr Asn Ser Gly
35 40 45
Gln Thr Ser Leu Leu Gly Thr Arg Ala Gly Thr Ser Phe Pro Gly Asn
50 55 60
Asp Tyr Gly Leu Ile Arg His Ser Asn Ala Ser Ala Ala Asp Gly Arg
65 70 75 80
Val Tyr Leu Tyr Asn Gly Ser Tyr Arg Asp Ile Thr Gly Ala Gly Asn
85 90 95
Ala Tyr Val Gly Gln Thr Val Gln Arg Ser Gly Ser Thr Thr Gly Leu
100 105 110
His Ser Gly Arg Val Thr Gly Leu Asn Ala Thr Val Asn Tyr Gly Gly
115 120 125
Gly Asp Ile Val Ser Gly Leu Ile Gln Thr Asn Val Cys Ala Glu Pro
130 135 140
Gly Asp Ser Gly Gly Ala Leu Phe Ala Gly Ser Thr Ala Leu Gly Leu
145 150 155 160
Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr
165 170

<210> 21

<211> 188

<212> PRT

<213> Streptomyces lividans

<400> 21

Asn Lys Leu Ile Gln Gly Gly Asp Ala Ile Tyr Ala Ser Ser Trp Arg
1 5 10 15
Cys Ser Leu Gly Phe Asn Val Arg Thr Ser Ser Gly Ala Glu Tyr Phe
20 25 30
Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Ala Trp Arg Ala Ser
35 40 45
Ser Gly Gly Thr Val Ile Gly Gln Thr Ala Gly Ser Ser Phe Pro Gly
50 55 60
Asn Asp Tyr Gly Ile Val Gln Tyr Thr Gly Ser Val Ser Arg Pro Gly
65 70 75 80
Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val Gly
85 90 95
Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly Arg
100 105 110
Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Gly Asp Val Val
115 120 125
Gly Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
130 135 140
Gly Ser Leu Tyr Gly Ser Asn Gly Thr Ala Tyr Gly Leu Thr Ser Gly
145 150 155 160
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val
165 170 175
Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr
180 185

<210> 22
 <211> 188
 <212> PRT
 <213> Streptomyces coelicolor

<400> 22

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Asn Lys Leu Ile Gln Gly Gly Asp Ala Ile Tyr Ala Ser Ser Trp Arg
1      5      10      15
Cys Ser Leu Gly Phe Asn Val Arg Thr Ser Ser Gly Ala Glu Tyr Phe
      20      25      30
Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Ala Trp Arg Ala Ser
      35      40      45
Ser Gly Gly Thr Val Ile Gly Gln Thr Ala Gly Ser Ser Phe Pro Gly
      50      55      60
Asn Asp Tyr Gly Ile Val Gln Tyr Thr Gly Ser Val Ser Arg Pro Gly
65      70      75      80
Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val Gly
      85      90      95
Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly Arg
      100      105      110
Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Gly Asp Val Val
      115      120      125
Gly Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
      130      135      140
Gly Ser Leu Tyr Gly Ser Asn Gly Thr Ala Tyr Gly Leu Thr Ser Gly
145      150      155      160
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val
      165      170      175
Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr
      180      185

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<210> 23
 <211> 189
 <212> PRT
 <213> Streptomyces albogriseolus

<400> 23

```

Thr Lys Leu Ile Gln Gly Gly Asp Ala Ile Tyr Ala Ser Ser Trp Arg
1      5      10      15
Cys Ser Leu Gly Phe Asn Val Arg Ser Ser Ser Gly Val Asp Tyr Phe
      20      25      30
Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Thr Trp Tyr Ser Asn
      35      40      45
Ser Ala Arg Thr Thr Ala Ile Gly Ser Thr Ala Gly Ser Ser Phe Pro
      50      55      60
Gly Asn Asp Tyr Gly Ile Val Arg Tyr Thr Gly Ser Val Ser Arg Pro
65      70      75      80
Gly Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val
      85      90      95
Gly Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly
      100      105      110
Arg Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Gly Asp Ile
      115      120      125
Val Ser Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser

```

130		135		140
Gly Gly Pro Leu Tyr	Gly Ser Asn Gly Thr	Ala Tyr Gly Leu Thr Ser		
145	150	155		160
Gly Gly Ser Gly Asn Cys Ser Ser	Gly Gly Thr Thr Phe Phe Gln Pro			
	165	170		175
Val Thr Glu Ala Leu Ser Ala Tyr	Gly Val Ser Val Tyr			
	180	185		

<210> 24
 <211> 188
 <212> PRT
 <213> Streptomyces griseus

<400> 24

Thr Lys Leu Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg	
1	5 10 15
Cys Ser Leu Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu	
	20 25 30
Thr Ala Gly His Cys Thr Asp Gly Ala Thr Thr Trp Trp Ala Asn Ser	
	35 40 45
Ala Arg Thr Thr Val Leu Gly Thr Thr Ser Gly Ser Ser Phe Pro Asn	
	50 55 60
Asn Asp Tyr Gly Ile Val Arg Tyr Thr Asn Thr Thr Ile Pro Lys Asp	
65	70 75 80
Gly Thr Val Gly Gly Gln Asp Ile Thr Ser Ala Ala Asn Ala Thr Val	
	85 90 95
Gly Met Ala Val Thr Arg Arg Gly Ser Thr Thr Gly Thr His Ser Gly	
	100 105 110
Ser Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Gly Asp Val	
	115 120 125
Val Tyr Gly Met Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser	
	130 135 140
Gly Gly Pro Leu Tyr Ser Gly Thr Arg Ala Ile Gly Leu Thr Ser Gly	
145	150 155 160
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val	
	165 170 175
Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr	
	180 185

<210> 25
 <211> 188
 <212> PRT
 <213> Streptomyces griseus

<400> 25

Val Leu Gly Gly Gly Ala Ile Tyr Gly Gly Gly Ser Arg Cys Ser Ala	
1	5 10 15
Ala Phe Asn Val Thr Lys Gly Gly Ala Arg Tyr Phe Val Thr Ala Gly	
	20 25 30
His Cys Thr Asn Ile Ser Ala Asn Trp Ser Ala Ser Ser Gly Gly Ser	
	35 40 45
Val Val Gly Val Arg Glu Gly Thr Ser Phe Pro Thr Asn Asp Tyr Gly	
	50 55 60
Ile Val Arg Tyr Thr Asp Gly Ser Ser Pro Ala Gly Thr Val Asp Leu	
65	70 75 80

Tyr Asn Gly Ser Thr Gln Asp Ile Ser Ser Ala Ala Asn Ala Val Val
 85 90 95
 Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val Thr Ser Gly
 100 105 110
 Thr Val Thr Ala Val Asn Val Thr Val Asn Tyr Gly Asp Gly Pro Val
 115 120 125
 Tyr Asn Met Gly Arg Thr Thr Ala Cys Ser Ala Gly Gly Asp Ser Gly
 130 135 140
 Gly Ala His Phe Ala Gly Ser Val Ala Leu Gly Ile His Ser Gly Ser
 145 150 155 160
 Ser Gly Cys Ser Gly Thr Ala Gly Ser Ala Ile His Gln Pro Val Thr
 165 170 175
 Lys Ala Leu Ser Ala Tyr Gly Val Thr Val Tyr Leu
 180 185

<210> 26
 <211> 190
 <212> PRT
 <213> Streptomyces fradiae

<400> 26

Gln Arg Glu Val Ala Gly Gly Asp Ala Ile Tyr Gly Gly Gly Ser Arg
 1 5 10 15
 Cys Ser Ala Ala Phe Asn Val Thr Lys Asn Gly Val Arg Tyr Phe Leu
 20 25 30
 Thr Ala Gly His Cys Thr Asn Leu Ser Ser Thr Trp Ser Ser Thr Ser
 35 40 45
 Gly Gly Thr Ser Ile Gly Val Arg Glu Gly Thr Ser Phe Pro Thr Asn
 50 55 60
 Asp Tyr Gly Ile Val Arg Tyr Thr Thr Thr Thr Asn Val Asp Gly Arg
 65 70 75 80
 Val Asn Leu Tyr Asn Gly Gly Tyr Gln Asp Ile Ala Ser Ala Ala Asp
 85 90 95
 Ala Val Val Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val
 100 105 110
 Thr Ser Gly Thr Val Ser Ala Val Asn Val Thr Val Asn Tyr Ser Asp
 115 120 125
 Gly Pro Val Tyr Gly Met Val Arg Thr Thr Ala Cys Ser Ala Gly Gly
 130 135 140
 Asp Ser Gly Gly Ala His Phe Ala Gly Ser Val Ala Leu Gly Ile His
 145 150 155 160
 Ser Gly Ser Ser Gly Cys Thr Gly Thr Asn Gly Ser Ala Ile His Gln
 165 170 175
 Pro Val Arg Glu Ala Leu Ser Ala Tyr Gly Val Asn Val Tyr
 180 185 190

<210> 27
 <211> 190
 <212> PRT
 <213> Streptomyces albogriseolus

<400> 27

Lys Pro Phe Ile Ala Gly Gly Asp Ala Ile Thr Gly Asn Gly Gly Arg
 1 5 10 15
 Cys Ser Leu Gly Phe Asn Val Thr Lys Gly Gly Glu Pro His Phe Leu

<213> Streptomyces griseus

<400> 29

Thr Pro Leu Ile Ala Gly Gly Asp Ala Ile Trp Gly Ser Gly Ser Arg
1 5 10 15
Cys Ser Leu Gly Phe Asn Val Val Lys Gly Gly Glu Pro Tyr Phe Leu
20 25 30
Thr Ala Gly His Cys Thr Glu Ser Val Thr Ser Trp Ser Asp Thr Gln
35 40 45
Gly Gly Ser Glu Ile Gly Ala Asn Glu Gly Ser Ser Phe Pro Glu Asn
50 55 60
Asp Tyr Gly Leu Val Lys Tyr Thr Ser Asp Thr Ala His Pro Ser Glu
65 70 75 80
Val Asn Leu Tyr Asp Gly Ser Thr Gln Ala Ile Thr Gln Ala Gly Asp
85 90 95
Ala Thr Val Gly Gln Ala Val Thr Arg Ser Gly Ser Thr Thr Gln Val
100 105 110
His Asp Gly Glu Val Thr Ala Leu Asp Ala Thr Val Asn Tyr Gly Asn
115 120 125
Gly Asp Ile Val Asn Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro
130 135 140
Gly Asp Ser Gly Gly Ala Leu Phe Ala Gly Asp Thr Ala Leu Gly Leu
145 150 155 160
Thr Ser Gly Gly Ser Gly Asp Cys Ser Ser Gly Gly Thr Thr Phe Phe
165 170 175
Gln Pro Val Pro Glu Ala Leu Ala Ala Tyr Gly Ala Glu Ile Gly
180 185 190

<210> 30

<211> 200

<212> PRT

<213> Streptomyces lividans

<400> 30

Lys Thr Phe Ala Ser Gly Gly Asp Ala Ile Phe Gly Gly Gly Ala Arg
1 5 10 15
Cys Ser Leu Gly Phe Asn Val Thr Ala Gly Asp Gly Ser Ala Ala Phe
20 25 30
Leu Thr Arg Gly His Cys Gly Gly Gly Ala Thr Met Trp Ser Asp Ala
35 40 45
Gln Gly Gly Gln Pro Ile Ala Thr Val Asp Gln Ala Val Phe Pro Pro
50 55 60
Glu Gly Asp Phe Gly Leu Val Arg Tyr Asp Gly Pro Ser Thr Glu Ala
65 70 75 80
Pro Ser Glu Val Asp Leu Gly Asp Gln Thr Leu Pro Ile Ser Gly Ala
85 90 95
Ala Glu Ala Ser Val Gly Gln Glu Val Phe Arg Met Gly Ser Thr Thr
100 105 110
Gly Leu Ala Asp Gly Gln Val Leu Gly Leu Asp Val Thr Val Asn Tyr
115 120 125
Pro Glu Gly Thr Val Thr Gly Leu Ile Gln Thr Asp Val Cys Ala Glu
130 135 140
Pro Gly Asp Ser Gly Gly Ser Leu Phe Thr Arg Asp Gly Leu Ala Ile
145 150 155 160
Arg Leu Thr Ser Gly Gly Thr Arg Asp Cys Thr Ser Gly Gly Glu Thr

165 170 175
 Phe Phe Gln Pro Val Thr Thr Ala Leu Ala Ala Val Gly Gly Thr Leu
 180 185 190
 Gly Gly Glu Asp Gly Gly Asp Gly
 195 200

<210> 31
 <211> 201
 <212> PRT
 <213> Streptomyces coelicolor

<400> 31

Lys Thr Phe Ala Ser Gly Gly Asp Ala Ile Phe Gly Gly Gly Ala Arg
 1 5 10 15
 Cys Ser Leu Gly Phe Asn Val Thr Ala Gly Asp Gly Ser Pro Ala Phe
 20 25 30
 Leu Thr Ala Gly His Cys Gly Val Ala Ala Asp Gln Trp Ser Asp Ala
 35 40 45
 Gln Gly Gly Gln Pro Ile Ala Thr Val Asp Gln Ala Val Phe Pro Gly
 50 55 60
 Glu Gly Asp Phe Ala Leu Val Arg Tyr Asp Asp Pro Ala Thr Glu Ala
 65 70 75 80
 Pro Ser Glu Val Asp Leu Gly Asp Gln Thr Leu Pro Ile Ser Gly Ala
 85 90 95
 Ala Glu Ala Ala Val Gly Gln Glu Val Phe Arg Met Gly Ser Thr Thr
 100 105 110
 Gly Leu Ala Asp Gly Gln Val Leu Gly Leu Asp Ala Thr Val Asn Tyr
 115 120 125
 Pro Glu Gly Met Val Thr Gly Leu Ile Gln Thr Asp Val Cys Ala Glu
 130 135 140
 Pro Gly Asp Ser Gly Gly Ser Leu Phe Thr Arg Asp Gly Leu Ala Ile
 145 150 155 160
 Gly Leu Thr Ser Gly Gly Ser Gly Asp Cys Thr Val Gly Gly Glu Thr
 165 170 175
 Phe Phe Gln Pro Val Thr Thr Ala Leu Ala Ala Val Gly Ala Thr Leu
 180 185 190
 Gly Gly Glu Asp Gly Gly Ala Gly Ala
 195 200

<210> 32
 <211> 68
 <212> PRT
 <213> Streptomyces platensis

<400> 32

Val Asp Gly Leu Ile Gln Thr Asp Val Cys Ala Glu Pro Gly Asp Ser
 1 5 10 15
 Gly Gly Ala Leu Phe Asp Gly Asp Ala Ala Ile Gly Leu Thr Ser Gly
 20 25 30
 Gly Ser Gly Asp Cys Ser Gln Gly Gly Glu Thr Phe Phe Gln Pro Val
 35 40 45
 Thr Glu Ala Leu Lys Ala Tyr Gly Ala Gln Ile Gly Gly Gly Gln Gly
 50 55 60
 Glu Pro Pro Glu
 65

<210> 33
 <211> 201
 <212> PRT
 <213> Streptomyces coelicolor

<400> 33

```

Thr Thr Arg Leu Asn Gly Ala Glu Pro Ile Leu Ser Thr Ala Gly Arg
1      5      10      15
Cys Ser Ala Gly Phe Asn Val Thr Asp Gly Thr Ser Asp Phe Ile Leu
      20      25      30
Thr Ala Gly His Cys Gly Pro Thr Gly Ser Val Trp Phe Gly Asp Arg
      35      40      45
Pro Gly Asp Gly Gln Val Gly Arg Thr Val Ala Gly Ser Phe Pro Gly
      50      55      60
Asp Asp Phe Ser Leu Val Glu Tyr Ala Asn Gly Lys Ala Gly Asp Gly
65      70      75      80
Ala Asp Val Val Ala Val Gly Asp Gly Lys Gly Val Arg Ile Thr Gly
      85      90      95
Ala Gly Glu Pro Ala Val Gly Gln Arg Val Phe Arg Ser Gly Ser Thr
      100     105     110
Ser Gly Leu Arg Asp Gly Arg Val Thr Ala Leu Asp Ala Thr Val Asn
      115     120     125
Tyr Pro Glu Gly Thr Val Thr Gly Leu Ile Glu Thr Asp Val Cys Ala
      130     135     140
Glu Pro Gly Asp Ser Gly Gly Pro Met Phe Ser Glu Gly Val Ala Leu
145     150     155     160
Gly Val Thr Ser Gly Gly Ser Gly Asp Cys Ala Lys Gly Gly Thr Thr
      165     170     175
Phe Phe Gln Pro Leu Pro Glu Ala Met Ala Ser Leu Gly Val Arg Leu
      180     185     190
Ile Val Pro Gly Arg Glu Gly Ala Ala
      195     200

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<210> 34
 <211> 188
 <212> PRT
 <213> Metarhizium anisopliae

<400> 34

```

Ala Thr Val Gln Gly Gly Asp Val Tyr Tyr Ile Asn Arg Ser Ser Arg
1      5      10      15
Cys Ser Ile Gly Phe Ala Val Thr Thr Gly Phe Val Ser Ala Gly His
      20      25      30
Cys Gly Gly Ser Gly Ala Ser Ala Thr Thr Ser Ser Gly Glu Ala Leu
      35      40      45
Gly Thr Phe Ser Gly Ser Val Phe Pro Gly Ser Ala Asp Met Ala Tyr
      50      55      60
Val Arg Thr Val Ser Gly Thr Val Leu Arg Gly Tyr Ile Asn Gly Tyr
65      70      75      80
Gly Gln Gly Ser Phe Pro Val Ser Gly Ser Ser Glu Ala Ala Val Gly
      85      90      95
Ala Ser Ile Cys Arg Ser Gly Ser Thr Thr Gln Val His Cys Gly Thr
      100     105     110
Ile Gly Ala Lys Gly Ala Thr Val Asn Tyr Pro Gln Gly Ala Val Ser

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	115					120						125					
Gly	Leu	Thr	Arg	Thr	Ser	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	Gly		
	130					135					140						
Ser	Phe	Tyr	Ser	Gly	Ser	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly	Ser		
145					150					155					160		
Gly	Asp	Cys	Ser	Arg	Gly	Gly	Thr	Thr	Tyr	Phe	Gln	Pro	Val	Asn	Arg		
				165					170					175			
Ile	Leu	Gln	Thr	Tyr	Gly	Leu	Thr	Leu	Val	Thr	Ala						
			180					185									

<210> 35
 <211> 195
 <212> PRT
 <213> Streptomyces griseus

<400> 35

Ala	Asp	Ile	Arg	Gly	Gly	Asp	Ala	Tyr	Tyr	Met	Asn	Gly	Ser	Gly	Arg		
1				5					10					15			
Cys	Ser	Val	Gly	Phe	Ser	Val	Thr	Arg	Gly	Thr	Gln	Asn	Gly	Phe	Ala		
			20					25					30				
Thr	Ala	Gly	His	Cys	Gly	Arg	Val	Gly	Thr	Thr	Thr	Asn	Gly	Val	Asn		
		35				40						45					
Gln	Gln	Ala	Gln	Gly	Thr	Phe	Gln	Gly	Ser	Thr	Phe	Pro	Gly	Arg	Asp		
50						55					60						
Ile	Ala	Trp	Val	Ala	Thr	Asn	Ala	Asn	Trp	Thr	Pro	Arg	Pro	Leu	Val		
65					70				75					80			
Asn	Gly	Tyr	Gly	Arg	Gly	Asp	Val	Thr	Val	Ala	Gly	Ser	Thr	Ala	Ser		
				85				90						95			
Val	Val	Gly	Ala	Ser	Val	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His		
			100					105					110				
Cys	Gly	Thr	Ile	Gln	Gln	Leu	Asn	Thr	Ser	Val	Thr	Tyr	Pro	Glu	Gly		
		115					120					125					
Thr	Ile	Ser	Gly	Val	Thr	Arg	Thr	Ser	Val	Cys	Ala	Glu	Pro	Gly	Asp		
130						135					140						
Ser	Gly	Gly	Ser	Tyr	Ile	Ser	Gly	Ser	Gln	Ala	Gln	Gly	Val	Thr	Ser		
145					150					155					160		
Gly	Gly	Ser	Gly	Asn	Cys	Ser	Ser	Gly	Gly	Thr	Thr	Tyr	Phe	Gln	Pro		
				165					170					175			
Ile	Asn	Pro	Leu	Leu	Gln	Ala	Tyr	Gly	Leu	Thr	Leu	Val	Thr	Ser	Gly		
			180					185						190			
Gly	Gly	Thr															
		195															

<210> 36
 <211> 197
 <212> PRT
 <213> Streptomyces coelicolor

<400> 36

Tyr	Asp	Leu	Arg	Gly	Gly	Glu	Ala	Tyr	Tyr	Ile	Asn	Asn	Ser	Ser	Arg		
1				5					10					15			
Cys	Ser	Ile	Gly	Phe	Pro	Ile	Thr	Lys	Gly	Thr	Gln	Gln	Gly	Phe	Ala		
			20					25					30				
Thr	Ala	Gly	His	Cys	Gly	Arg	Ala	Gly	Ser	Ser	Thr	Thr	Gly	Ala	Asn		
			35				40						45				

Arg Val Ala Gln Gly Thr Phe Gln Gly Ser Ile Phe Pro Gly Arg Asp
 50 55 60
 Met Ala Trp Val Ala Thr Asn Ser Ser Trp Thr Ala Thr Pro Tyr Val
 65 70 75 80
 Leu Gly Ala Gly Gly Gln Asn Val Gln Val Thr Gly Ser Thr Ala Ser
 85 90 95
 Pro Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His
 100 105 110
 Cys Gly Thr Val Thr Gln Leu Asn Thr Ser Val Thr Tyr Gln Glu Gly
 115 120 125
 Thr Ile Ser Pro Val Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp
 130 135 140
 Ser Gly Gly Ser Phe Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser
 145 150 155 160
 Gly Gly Ser Gly Asp Cys Arg Thr Gly Gly Glu Thr Phe Phe Gln Pro
 165 170 175
 Ile Asn Ala Leu Leu Gln Asn Tyr Gly Leu Thr Leu Lys Thr Thr Gly
 180 185 190
 Gly Asp Asp Gly Gly
 195

<210> 37
 <211> 189
 <212> PRT
 <213> Streptomyces spp.

<400> 37

Tyr Asp Leu Val Gly Gly Asp Ala Tyr Tyr Ile Gly Asn Gly Arg Cys
 1 5 10 15
 Ser Ile Gly Phe Ser Val Arg Gln Gly Ser Thr Pro Gly Phe Val Thr
 20 25 30
 Ala Gly His Cys Gly Ser Val Gly Asn Ala Thr Thr Gly Phe Asn Arg
 35 40 45
 Val Ser Gln Gly Thr Phe Arg Gly Ser Trp Phe Pro Gly Arg Asp Met
 50 55 60
 Ala Trp Val Ala Val Asn Ser Asn Trp Thr Pro Thr Ser Leu Val Arg
 65 70 75 80
 Asn Ser Gly Ser Gly Val Arg Val Thr Gly Ser Thr Gln Ala Thr Val
 85 90 95
 Gly Ser Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly
 100 105 110
 Thr Ile Gln Gln His Asn Thr Ser Val Thr Tyr Pro Gln Gly Thr Ile
 115 120 125
 Thr Gly Val Thr Arg Thr Ser Ala Cys Ala Gln Pro Gly Asp Ser Gly
 130 135 140
 Gly Ser Phe Ile Ser Gly Thr Gln Ala Gln Gly Val Thr Ser Gly Gly
 145 150 155 160
 Ser Gly Asn Cys Ser Ile Gly Gly Thr Thr Phe His Gln Pro Val Asn
 165 170 175
 Pro Ile Leu Ser Gln Tyr Gly Leu Thr Leu Val Arg Ser
 180 185

<210> 38
 <211> 187
 <212> PRT
 <213> Streptomyces spp.

<400> 38

Tyr Asp Leu Val Gly Gly Asp Ala Tyr Tyr Met Gly Gly Gly Arg Cys
1 5 10 15
Ser Val Gly Phe Ser Val Thr Gln Gly Ser Thr Pro Gly Phe Ala Thr
20 25 30
Ala Gly His Cys Gly Thr Val Gly Thr Ser Thr Thr Gly Tyr Asn Gln
35 40 45
Ala Ala Gln Gly Thr Phe Glu Glu Ser Ser Phe Pro Gly Asp Asp Met
50 55 60
Ala Trp Val Ser Val Asn Ser Asp Trp Asn Thr Thr Pro Thr Val Asn
65 70 75 80
Glu Gly Glu Val Thr Val Ser Gly Ser Thr Glu Ala Ala Val Gly Ala
85 90 95
Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile
100 105 110
Gln Gln His Asn Thr Ser Val Thr Tyr Pro Glu Gly Thr Ile Thr Gly
115 120 125
Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser
130 135 140
Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly
145 150 155 160
Asn Cys Thr Ser Gly Gly Thr Thr Tyr His Gln Pro Ile Asn Pro Leu
165 170 175
Leu Ser Ala Tyr Gly Leu Asp Leu Val Thr Gly
180 185

<210> 39

<211> 193

<212> PRT

<213> Streptomyces coelicolor

<400> 39

Glu Asp Leu Val Gly Gly Asp Ala Tyr Tyr Ile Asp Asp Gln Ala Arg
1 5 10 15
Cys Ser Ile Gly Phe Ser Val Thr Lys Asp Asp Gln Glu Gly Phe Ala
20 25 30
Thr Ala Gly His Cys Gly Asp Pro Gly Ala Thr Thr Thr Gly Tyr Asn
35 40 45
Glu Ala Asp Gln Gly Thr Phe Gln Ala Ser Thr Phe Pro Gly Lys Asp
50 55 60
Met Ala Trp Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val
65 70 75 80
Lys Ala Glu Gly Gly Glu Lys Ile Gln Leu Ala Gly Ser Val Glu Ala
85 90 95
Leu Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His
100 105 110
Cys Gly Thr Ile Gln Gln His Asp Thr Ser Val Thr Tyr Pro Glu Gly
115 120 125
Thr Val Asp Gly Leu Thr Glu Thr Thr Val Cys Ala Glu Pro Gly Asp
130 135 140
Ser Gly Gly Pro Phe Val Ser Gly Val Gln Ala Gln Gly Thr Thr Ser
145 150 155 160
Gly Gly Ser Gly Asp Cys Thr Asn Gly Gly Thr Thr Phe Tyr Gln Pro
165 170 175

Val Asn Pro Leu Leu Ser Asp Phe Gly Leu Thr Leu Lys Thr Thr Ser
 180 185 190
 Ala

<210> 40
 <211> 187
 <212> PRT
 <213> Thermobifida fusca

<400> 40

Leu Ala Ala Ile Ile Gly Gly Asn Pro Tyr Tyr Phe Gly Asn Tyr Arg
 1 5 10 15
 Cys Ser Ile Gly Phe Ser Val Arg Gln Gly Ser Gln Thr Gly Phe Ala
 20 25 30
 Thr Ala Gly His Cys Gly Ser Thr Gly Thr Arg Val Ser Ser Pro Ser
 35 40 45
 Gly Thr Val Ala Gly Ser Tyr Phe Pro Gly Arg Asp Met Gly Trp Val
 50 55 60
 Arg Ile Thr Ser Ala Asp Thr Val Thr Pro Leu Val Asn Arg Tyr Asn
 65 70 75 80
 Gly Gly Thr Val Thr Val Thr Gly Ser Gln Glu Ala Ala Thr Gly Ser
 85 90 95
 Ser Val Cys Arg Ser Gly Ala Thr Thr Gly Trp Arg Cys Gly Thr Ile
 100 105 110
 Gln Ser Lys Asn Gln Thr Val Arg Tyr Ala Glu Gly Thr Val Thr Gly
 115 120 125
 Leu Thr Arg Thr Thr Ala Cys Ala Glu Gly Gly Asp Ser Gly Gly Pro
 130 135 140
 Trp Leu Thr Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Thr Gly
 145 150 155 160
 Asp Cys Arg Ser Gly Gly Ile Thr Phe Phe Gln Pro Ile Asn Pro Leu
 165 170 175
 Leu Ser Tyr Phe Gly Leu Gln Leu Val Thr Gly
 180 185

<210> 41
 <211> 198
 <212> PRT
 <213> Lysobacter enzymogenes

<400> 41

Ala Asn Ile Val Gly Gly Ile Glu Tyr Ser Ile Asn Asn Ala Ser Leu
 1 5 10 15
 Cys Ser Val Gly Phe Ser Val Thr Arg Gly Ala Thr Lys Gly Phe Val
 20 25 30
 Thr Ala Gly His Cys Gly Thr Val Asn Ala Thr Ala Arg Ile Gly Gly
 35 40 45
 Ala Val Val Gly Thr Phe Ala Ala Arg Val Phe Pro Gly Asn Asp Arg
 50 55 60
 Ala Trp Val Ser Leu Thr Ser Ala Gln Thr Leu Leu Pro Arg Val Ala
 65 70 75 80
 Asn Gly Ser Ser Phe Val Thr Val Arg Gly Ser Thr Glu Ala Ala Val
 85 90 95
 Gly Ala Ala Val Cys Arg Ser Gly Arg Thr Thr Gly Tyr Gln Cys Gly

			100					105					110				
Thr	Ile	Thr	Ala	Lys	Asn	Val	Thr	Ala	Asn	Tyr	Ala	Glu	Gly	Ala	Val		
			115					120					125				
Arg	Gly	Leu	Thr	Gln	Gly	Asn	Ala	Cys	Met	Gly	Arg	Gly	Asp	Ser	Gly		
			130				135						140				
Gly	Ser	Trp	Ile	Thr	Ser	Ala	Gly	Gln	Ala	Gln	Gly	Val	Met	Ser	Gly		
145						150					155				160		
Gly	Asn	Val	Gln	Ser	Asn	Gly	Asn	Asn	Cys	Gly	Ile	Pro	Ala	Ser	Gln		
				165					170						175		
Arg	Ser	Ser	Leu	Phe	Glu	Arg	Leu	Gln	Pro	Ile	Leu	Ser	Gln	Tyr	Gly		
			180					185					190				
Leu	Ser	Leu	Val	Thr	Gly												
			195														

<210> 42
 <211> 189
 <212> PRT
 <213> Streptomyces coelicolor

<400> 42

Ala	Ala	Gly	Thr	Val	Gly	Gly	Asp	Pro	Tyr	Tyr	Thr	Gly	Asn	Val	Arg		
1				5					10					15			
Cys	Ser	Ile	Gly	Phe	Ser	Val	His	Gly	Gly	Phe	Val	Thr	Ala	Gly	His		
			20					25					30				
Cys	Gly	Arg	Ala	Gly	Ala	Gly	Val	Ser	Gly	Trp	Asp	Arg	Ser	Tyr	Ile		
		35					40					45					
Gly	Thr	Phe	Gln	Gly	Ser	Ser	Phe	Pro	Asp	Asn	Asp	Tyr	Ala	Trp	Val		
50						55					60						
Ser	Val	Gly	Ser	Gly	Trp	Trp	Thr	Val	Pro	Val	Val	Leu	Gly	Trp	Gly		
65					70					75					80		
Thr	Val	Ser	Asp	Gln	Leu	Val	Arg	Gly	Ser	Asn	Val	Ala	Pro	Val	Gly		
				85					90					95			
Ala	Ser	Ile	Cys	Arg	Ser	Gly	Ser	Thr	His	Trp	His	Cys	Gly	Thr			
			100					105					110				
Val	Leu	Ala	His	Asn	Glu	Thr	Val	Asn	Tyr	Ser	Asp	Gly	Ser	Val	Val		
		115					120					125					
His	Gln	Leu	Thr	Lys	Thr	Ser	Val	Cys	Ala	Glu	Gly	Gly	Asp	Ser	Gly		
		130					135					140					
Gly	Ser	Phe	Ile	Ser	Gly	Asp	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly		
145					150					155					160		
Trp	Gly	Asn	Cys	Ser	Ser	Gly	Gly	Glu	Thr	Trp	Phe	Gln	Pro	Val	Asn		
			165					170						175			
Glu	Ile	Leu	Asn	Arg	Tyr	Gly	Leu	Thr	Leu	His	Thr	Ala					
			180					185									

<210> 43
 <211> 197
 <212> PRT
 <213> Rarobacter faecitabidus

<400> 43

Val	Ile	Val	Pro	Val	Arg	Asp	Tyr	Trp	Gly	Gly	Asp	Ala	Leu	Ser	Gly		
1				5					10					15			
Cys	Thr	Leu	Ala	Phe	Pro	Val	Tyr	Gly	Gly	Phe	Leu	Thr	Ala	Gly	His		
			20					25					30				

Cys Ala Val Glu Gly Lys Gly His Ile Leu Lys Thr Glu Met Thr Gly
 35 40 45
 Gly Gln Ile Gly Thr Val Glu Ala Ser Gln Phe Gly Asp Gly Ile Asp
 50 55 60
 Ala Ala Trp Ala Lys Asn Tyr Gly Asp Trp Asn Gly Arg Gly Arg Val
 65 70 75 80
 Thr His Trp Asn Gly Gly Gly Gly Val Asp Ile Lys Gly Ser Asn Glu
 85 90 95
 Ala Ala Val Gly Ala His Met Cys Lys Ser Gly Arg Thr Thr Lys Trp
 100 105 110
 Thr Cys Gly Tyr Leu Leu Arg Lys Asp Val Ser Val Asn Tyr Gly Asn
 115 120 125
 Gly His Ile Val Thr Leu Asn Glu Thr Ser Ala Cys Ala Leu Gly Gly
 130 135 140
 Asp Ser Gly Gly Ala Tyr Val Trp Asn Asp Gln Ala Gln Gly Ile Thr
 145 150 155 160
 Ser Gly Ser Asn Met Asp Thr Asn Asn Cys Arg Ser Phe Tyr Gln Pro
 165 170 175
 Val Asn Thr Val Leu Asn Lys Trp Lys Leu Ser Leu Val Thr Ser Thr
 180 185 190
 Asp Val Thr Thr Ser
 195

<210> 44
 <211> 191
 <212> PRT
 <213> Streptomyces coelicolor

<400> 44

Asp Pro Pro Leu Arg Ser Gly Leu Ala Ile Tyr Gly Thr Asn Val Arg
 1 5 10 15
 Cys Ser Ser Ala Phe Met Ala Tyr Ser Gly Ser Ser Tyr Tyr Met Met
 20 25 30
 Thr Ala Gly His Cys Ala Glu Asp Ser Ser Tyr Trp Glu Val Pro Thr
 35 40 45
 Tyr Ser Tyr Gly Tyr Gln Gly Val Gly His Val Ala Asp Tyr Thr Phe
 50 55 60
 Gly Tyr Tyr Gly Asp Ser Ala Ile Val Arg Val Asp Asp Pro Gly Phe
 65 70 75 80
 Trp Gln Pro Arg Gly Trp Val Tyr Pro Ser Thr Arg Ile Thr Asn Trp
 85 90 95
 Asp Tyr Asp Tyr Val Gly Gln Tyr Val Cys Lys Gln Gly Ser Thr Thr
 100 105 110
 Gly Tyr Thr Cys Gly Gln Ile Thr Glu Thr Asn Ala Thr Val Ser Tyr
 115 120 125
 Pro Gly Arg Thr Leu Thr Gly Met Thr Trp Ser Thr Ala Cys Asp Ala
 130 135 140
 Pro Gly Asp Ser Gly Ser Gly Val Tyr Asp Gly Ser Thr Ala His Gly
 145 150 155 160
 Ile Leu Ser Gly Gly Pro Asn Ser Gly Cys Gly Met Ile His Glu Pro
 165 170 175
 Ile Ser Arg Ala Leu Ala Asp Arg Gly Val Thr Leu Leu Ala Gly
 180 185 190

<210> 45
 <211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 45
tgcgccgagc ccggcgactc

20

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 46
gagtcgccgg gctcggcgca

20

<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 47
ttccccggca acgactacgc gtgggt

26

<210> 48
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 48
acccacgcgt agtcgttgcc ggggaa

26

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 49
gccgctgctc gatcgggttc

20

<210> 50
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 50
gcagttgccg gagccgccgg acgt

24

<210> 51
<211> 14
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<400> 51
tsggsgncrt gggt

14

<210> 52
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 52

Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro
1 5 10

<210> 53
<211> 555
<212> DNA
<213> Cellulomonas flavigena

<400> 53
gtcgacgtca tcgggggcaa cgcgtactac atcgggtcgc gctcgcggtg ctcgatcggg 60
ttcgcggtcg agggcggtt cgtcaccgcg gggcactcgc ggcgcgcggg cgcgagcacg 120
tcgtcaccgt cggggacatt ccgcggctcg tcgttccccg gcaacgacta cgcgtgggtc 180
caggtcgcct cgggcaaacac gccgcgcggg ctggtgaaca accactcggg cggcacggtg 240
cgcgtaaccg gctcgcagca ggccgcggtc ggctcgtacg tgtgccgatc gggcagcacg 300
acgggatggc ggtgcggcta cgtccgggcg tacaacacga ccgtgcggta cgcggagggc 360
tcggtctcgg gcctcatccg cagcagcgtg tgcgccgagc cgggcgactc cggcggctcg 420
ctggtcgcgc gcacgcaggc ccagggcgtc acgtcgggcg ggtccggcaa ctgccgctac 480
gggggcacga cgtacttcca gcccggtgaac gagatcctgc aggaccagcc cgggccgctc 540
accacgcgtg cccta 555

<210> 54
 <211> 185
 <212> PRT
 <213> Cellulomonas flavigena

<400> 54

Val	Asp	Val	Ile	Gly	Gly	Asn	Ala	Tyr	Tyr	Ile	Gly	Ser	Arg	Ser	Arg
1				5					10					15	
Cys	Ser	Ile	Gly	Phe	Ala	Val	Glu	Gly	Gly	Phe	Val	Thr	Ala	Gly	His
		20						25					30		
Cys	Gly	Arg	Ala	Gly	Ala	Ser	Thr	Ser	Ser	Pro	Ser	Gly	Thr	Phe	Arg
	35						40					45			
Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala	Trp	Val	Gln	Val	Ala	Ser
	50					55					60				
Gly	Asn	Thr	Pro	Arg	Gly	Leu	Val	Asn	Asn	His	Ser	Gly	Gly	Thr	Val
65					70					75					80
Arg	Val	Thr	Gly	Ser	Gln	Gln	Ala	Ala	Val	Gly	Ser	Tyr	Val	Cys	Arg
					85				90					95	
Ser	Gly	Ser	Thr	Thr	Gly	Trp	Arg	Cys	Gly	Tyr	Val	Arg	Ala	Tyr	Asn
			100					105					110		
Thr	Thr	Val	Arg	Tyr	Ala	Glu	Gly	Ser	Val	Ser	Gly	Leu	Ile	Arg	Thr
		115					120					125			
Ser	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	Gly	Ser	Leu	Val	Ala	Gly
	130					135					140				
Thr	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly	Ser	Gly	Asn	Cys	Arg	Tyr
145					150					155					160
Gly	Gly	Thr	Thr	Tyr	Phe	Gln	Pro	Val	Asn	Glu	Ile	Leu	Gln	Asp	Gln
				165					170					175	
Pro	Gly	Pro	Ser	Thr	Thr	Arg	Ala	Leu							
			180					185							

<210> 55
 <211> 1009
 <212> DNA
 <213> Cellulomonas biazotea

<400> 55

taaaacagac	ggccagtgaa	tttgtaatac	gactcactat	aggcgaattg	aatttagcgg	60
ccgcgaattc	gcccttacct	atagggcacg	cgtggtcgac	ggccctgggc	tggtacgtcg	120
acgtcactac	caacacggtc	gtcgtcaacg	ccaccgccct	cgccgtggcc	caggcgaccg	180
agatcgtcgc	cgccgcaacg	gtgcccggcg	acgccgtccg	ggtcgtcgag	accaccgagg	240
cgccccgcac	gttcatcgac	gtcatcggcg	gcaaccgtta	ccggatcaac	aacacctcgc	300
gctgctcggg	cggttccgcc	gtcagcggcg	gcttcgtcac	cgccggggcac	tgcgggcacga	360
ccggcgcgac	cacgacgaaa	ccgtccggca	cgttcgccgg	ctcgtcgttc	cccggcaacg	420
actacgcgtg	ggtgcgcgtc	gcgtccggca	acaccccggt	cggcgccgtg	aacaactaca	480
gcggcggcac	cgtggccgtc	gccggctcga	cgcaggcgac	cgtcggtgcg	tccgtctgcc	540
gctccggctc	caccacgggg	tggcgtcgcg	ggaatgatcca	ggcgttcaac	tccaccgtca	600
actacgcgca	gggcagcgtc	tccggcctca	tccgcacgaa	cgtgtgcgcc	gagcccggcg	660
actccggcgg	ctcgtctcatc	gccggcaacc	aggcccaggg	cctgacgtcc	ggcgggtcgg	720
gcaactgcac	caccggcggg	acgacgtact	tccagcccgt	caacgaggcg	ctctccgcct	780
acggcctgac	gctcgtcacg	tcgtccggcg	gcggcggttg	cggcggcacg	acctgcaccg	840
ggtacgcgcg	gacctacacc	ggctcgtctc	cctcgcggca	gtccgccgtc	cagccgtccg	900
gcagctatgt	gaccgtcggg	tccagcggca	ccatccgcgt	ctgcctcgac	ggcccagcgc	960
ggacggactt	cgacctgtac	ctgcagaagt	ggaacgggtc	cgcgtgggc		1009

<210> 56

<211> 335
 <212> PRT
 <213> Cellulomonas biazotea

<400> 56

```

Lys Gln Thr Ala Ser Glu Phe Val Ile Arg Leu Thr Ile Gly Glu Leu
1      5      10      15
Asn Leu Ala Ala Asn Ser Pro Leu Pro Ile Gly His Ala Trp Ser
      20      25      30
Thr Ala Leu Gly Trp Tyr Val Asp Val Thr Thr Asn Thr Val Val Val
      35      40      45
Asn Ala Thr Ala Leu Ala Val Ala Gln Ala Thr Glu Ile Val Ala Ala
      50      55      60
Ala Thr Val Pro Ala Asp Ala Val Arg Val Val Glu Thr Thr Glu Ala
65      70      75      80
Pro Arg Thr Phe Ile Asp Val Ile Gly Gly Asn Arg Tyr Arg Ile Asn
      85      90      95
Asn Thr Ser Arg Cys Ser Val Gly Phe Ala Val Ser Gly Gly Phe Val
      100     105     110
Thr Ala Gly His Cys Gly Thr Thr Gly Ala Thr Thr Thr Lys Pro Ser
      115     120     125
Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val
      130     135     140
Arg Val Ala Ser Gly Asn Thr Pro Val Gly Ala Val Asn Asn Tyr Ser
145     150     155     160
Gly Gly Thr Val Ala Val Ala Gly Ser Thr Gln Ala Thr Val Gly Ala
      165     170     175
Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Thr Ile
      180     185     190
Gln Ala Phe Asn Ser Thr Val Asn Tyr Ala Gln Gly Ser Val Ser Gly

```

```

      195      200      205
Leu Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser
      210     215     220
Leu Ile Ala Gly Asn Gln Ala Gln Gly Leu Thr Ser Gly Gly Ser Gly
225     230     235     240
Asn Cys Thr Thr Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ala
      245     250     255
Leu Ser Ala Tyr Gly Leu Thr Leu Val Thr Ser Ser Gly Gly Gly Gly
      260     265     270
Gly Gly Gly Thr Thr Cys Thr Gly Tyr Ala Arg Thr Tyr Thr Gly Ser
      275     280     285
Leu Ala Ser Arg Gln Ser Ala Val Gln Pro Ser Gly Ser Tyr Val Thr
      290     295     300
Val Gly Ser Ser Gly Thr Ile Arg Val Cys Leu Asp Gly Pro Ser Gly
305     310     315     320
Thr Asp Phe Asp Leu Tyr Leu Gln Lys Trp Asn Gly Ser Ala Trp
      325     330     335

```

<210> 57
 <211> 474
 <212> DNA
 <213> Cellulomonas fimi

<400> 57

```

gtggacgtga tggggggcga cgcctactac atcggcggcc gcagccgctg ttcgatcggg 60
ttcgccgtca cggggggctt cgtgaccgcc gggcactgcg gccgcaccgg cgcgggccacg 120
acgagcccgt cgggcacgtt cgcgggctcg agcttcccgg gcaacgacta cgcgtggggtg 180
cgggtcgcg cgggcaacac gcccgtcggc gcggtgaaca actacagcgg cggcacggtc 240
gccgtcgccg gctcgaccca ggccgccgtc ggtgcgaccg tgtgccgctc gggctccacc 300
accggtggtc ggtgcggcac catccaggcg ttcaacgcga ccgtcaacta cggcgagggc 360
agcgtctccg gcctcatccg caccgaacgtg tgcgccgagc ccggcgactc gggcggctcg 420
ctcgtcgccg gcaaccaggc gcagggcatt acgtccggcg gtcgccgaaa ctgc 474

```

<210> 58
 <211> 144
 <212> PRT
 <213> Cellulomonas fimi

<400> 58

```

Val Asp Val Ile Gly Gly Asp Ala Tyr Tyr Ile Gly Gly Arg Ser Arg
1           5           10          15
Cys Ser Ile Gly Phe Ala Val Thr Gly Gly Phe Val Thr Ala Gly His
          20          25          30
Cys Gly Arg Thr Gly Ala Ala Thr Thr Ser Pro Ser Gly Thr Phe Ala
          35          40          45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Arg Val Ala Ser
          50          55          60
Gly Asn Thr Pro Val Gly Ala Val Asn Asn Tyr Ser Gly Gly Thr Val
65          70          75          80
Ala Val Ala Gly Ser Thr Gln Ala Ala Val Gly Ala Thr Val Cys Arg
          85          90          95
Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Thr Ile Gln Ala Phe Asn
          100         105         110
Ala Thr Val Asn Tyr Ala Glu Gly Ser Val Ser Gly Leu Ile Arg Thr
          115         120         125
Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Val Ala Gly
          130         135         140

```

<210> 59
 <211> 462
 <212> DNA
 <213> Cellulomonas gelida

<400> 59

```

ctcgcgggca accaggcgca gggcgtagcg tcggggcgggt cgggcaactg ctcgtcgggc 60
gggacgacgt acttccagcc cgtcaacgag gccctccggg tgtacgggct cacgctcgtg 120
acctctgacg gtggggggcac cgagccgccg ccgaccgggt gccagggcta tgcgcggacc 180
taccagggca gcgctctcggc cgggacgtcg gtcgcgcagc cgaacggttc gtacgtcacg 240
accggggggc ggacgcaccg ggtgtgcctg agcggaccgg cgggcacgga cctggacctg 300
tacctgcaga agtggaacgg gtactcgtgg gccagcgctg cgcagtcgac gtcgcctggt 360
gccacggagg cggtcacgta caccggggacc gccggctact accgctacgt ggtccacgcg 420
tacgcggggt cggggggcgta caccctgggg gcgacgaccc cg 462

```

<210> 60
 <211> 154
 <212> PRT
 <213> Cellulomonas gelida

<400> 60

Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn

1				5					10					15			
Cys	Ser	Ser	Gly	Gly	Thr	Thr	Tyr	Phe	Gln	Pro	Val	Asn	Glu	Ala	Leu		
			20					25					30				
Arg	Val	Tyr	Gly	Leu	Thr	Leu	Val	Thr	Ser	Asp	Gly	Gly	Gly	Thr	Glu		
		35					40					45					
Pro	Pro	Pro	Thr	Gly	Cys	Gln	Gly	Tyr	Ala	Arg	Thr	Tyr	Gln	Gly	Ser		
		50				55					60						
Val	Ser	Ala	Gly	Thr	Ser	Val	Ala	Gln	Pro	Asn	Gly	Ser	Tyr	Val	Thr		
65					70				75						80		
Thr	Gly	Gly	Gly	Thr	His	Arg	Val	Cys	Leu	Ser	Gly	Pro	Ala	Gly	Thr		
				85					90					95			
Asp	Leu	Asp	Leu	Tyr	Leu	Gln	Lys	Trp	Asn	Gly	Tyr	Ser	Trp	Ala	Ser		
			100					105					110				
Val	Ala	Gln	Ser	Thr	Ser	Pro	Gly	Ala	Thr	Glu	Ala	Val	Thr	Tyr	Thr		
		115					120					125					
Gly	Thr	Ala	Gly	Tyr	Tyr	Arg	Tyr	Val	Val	His	Ala	Tyr	Ala	Gly	Ser		
	130					135					140						
Gly	Ala	Tyr	Thr	Leu	Gly	Ala	Thr	Thr	Pro								
145					150												

<210> 61
 <211> 257
 <212> DNA
 <213> Cellulomonas iranensis

<400> 61	
ttccccggca acgactacgc gtgggtccag gtcgggtcgg gcgacacccc ccgcggcctg	60
gtcaacaact acgcggggcgg caccgtgcgg gtcaccgggt cgcagcaggc cgcggtcggc	120
gcgtacgtct gccggtcggg cagcacgacg ggctggcgct gcggcaccgt gcaggcctac	180
aacgcgtcgg tccgctacgc cgagggcacc gtctcgggcc tcatccgcac caacgtctgc	240
gccgagcccc gcgactc	257

<210> 62
 <211> 85
 <212> PRT
 <213> Cellulomonas iranensis

<400> 62

Phe	Pro	Gly	Asn	Asp	Tyr	Ala	Trp	Val	Gln	Val	Gly	Ser	Gly	Asp	Thr		
1				5				10					15				
Pro	Arg	Gly	Leu	Val	Asn	Asn	Tyr	Ala	Gly	Gly	Thr	Val	Arg	Val	Thr		
			20					25				30					
Gly	Ser	Gln	Gln	Ala	Ala	Val	Gly	Ala	Tyr	Val	Cys	Arg	Ser	Gly	Ser		
		35					40				45						
Thr	Thr	Gly	Trp	Arg	Cys	Gly	Thr	Val	Gln	Ala	Tyr	Asn	Ala	Ser	Val		
	50				55						60						
Arg	Tyr	Ala	Glu	Gly	Thr	Val	Ser	Gly	Leu	Ile	Arg	Thr	Asn	Val	Cys		
65					70				75						80		
Ala	Glu	Pro	Gly	Asp													
				85													

<210> 63
 <211> 904
 <212> DNA
 <213> Cellulomonas cellasea

<400> 63

```
gtcggggcggg tccggcaact gccgctacgg gggcacgacg tacttccagc ccgatgaacga      60
gatcctgcag gcctacggtc tgcgtctcgt cctgggctga cacgctcgcg gcggggcccg      120
ctcgacgcgg ccggcccgtc ggcccgggtc gccgcctggt acgtcgacgt gccgaccaac      180
aagctcgtcg tcgagtcggt cggcgacacc gcggcgggccg ccgacgccgt cgccgccgcg      240
ggcctgcctg ccgacgccgt gacgctcgcg accaccgagg cgccacggac gtctcgtcgac      300
gtcatcggcg gcaacgcgta ctacatcaac gcgagcagcc gctgctcggg cggcttcgcg      360
gtcgagggcg ggttcgtcac cgcgggccac tgcgggcgcg cgggcgcgag cacgtcgtca      420
ccgtcgggga ccttcgcgcg ctctcgtctc cccggcaacg actacgcgtg ggtccaggtc      480
gcctcgggca acacgccgcg cgggctggtg aacaaccact cgggcggcac ggtgcgcgtc      540
accggctcgc agcaggccgc ggtcggctcg tacgtgtgcc gatcgggcag cacgacggga      600
tggcggtgcg gctacgtccg ggcgtaaac acgaccgtgc ggtacgcgga gggctcggtc      660
tcgggcctca tccgcacgag cgtgtgcgcc gagccgggcg actccggcgg ctcgctggtc      720
gccggcacgc aggccaggcg cgtcacgtcg ggcggtccg gcaactgccg ctacgggggc      780
acgacgtact tccagcccgt gaacgagatc ctgcaggcct acggtctgcg tctcgtcctg      840
ggctgacacg ctcgcggcgg gccctccctt gcccgctcgc cgccggcccc accagcccgg      900
gccg                                     904
```

<210> 64

<211> 300

<212> PRT

<213> Cellulomonas cellasea

<400> 64

```
Val Gly Arg Val Arg Gln Leu Pro Leu Arg Gly His Asp Val Leu Pro
1      5      10      15
Ala Arg Glu Arg Asp Pro Ala Gly Leu Arg Ser Ala Ser Arg Pro Gly
20     25     30
Leu Thr Arg Ser Arg Arg Ala Arg Leu Asp Ala Ala Gly Pro Ser Ala
35     40     45
Arg Val Ala Ala Trp Tyr Val Asp Val Pro Thr Asn Lys Leu Val Val
50     55     60
Glu Ser Val Gly Asp Thr Ala Ala Ala Asp Ala Val Ala Ala Ala
65     70     75     80
Gly Leu Pro Ala Asp Ala Val Thr Leu Ala Thr Thr Glu Ala Pro Arg
85     90     95
Thr Phe Val Asp Val Ile Gly Gly Asn Ala Tyr Tyr Ile Asn Ala Ser
100    105    110
Ser Arg Cys Ser Val Gly Phe Ala Val Glu Gly Gly Phe Val Thr Ala
115    120    125
Gly His Cys Gly Arg Ala Gly Ala Ser Thr Ser Ser Pro Ser Gly Thr
130    135    140
Phe Arg Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Gln Val
145    150    155    160
Ala Ser Gly Asn Thr Pro Arg Gly Leu Val Asn Asn His Ser Gly Gly
165    170    175
Thr Val Arg Val Thr Gly Ser Gln Gln Ala Ala Val Gly Ser Tyr Val
180    185    190
Cys Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Tyr Val Arg Ala
195    200    205
Tyr Asn Thr Thr Val Arg Tyr Ala Glu Gly Ser Val Ser Gly Leu Ile
210    215    220
Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Val
225    230    235    240
Ala Gly Thr Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys
245    250    255
```

Arg Tyr Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ile Leu Gln
260 265 270
Ala Tyr Gly Leu Arg Leu Val Leu Gly His Ala Arg Gly Gly Pro Ser
275 280 285
Pro Ala Arg Arg Ala Pro Ala Pro Pro Ala Arg Ala
290 295 300

<210> 65
<211> 429
<212> DNA
<213> Cellulomonas xylanilytica

<400> 65
cgctgctcga tcgggttcgc cgtgacgggc ggcttcgtga ccgccggcca ctgcggacgg 60
tccggcgcca cgacgacgtc gccgagcggc acgttcgccg ggtccagctt tcccggcaac 120
gactacgcct gggtcgcgc gccctcgggc aacacgccgg tcggtgcggt gaaccgctac 180
gacggcagcc gggtgaccgt ggccgggtcc accgacgcgg ccgtcgggtgc cgcggctctgc 240
cggtcggggg cgacgaccgc gtgggggtgc ggcacgatcc agtcccgcgg cgcgagcgtc 300
acgtacgccc agggcaccgt cagcgggctc atccgcacca acgtgtgcgc cgagccgggt 360
gactccgggg ggtcgctgat cgcgggcacc caggcgcggg gcgtgacgtc cggcgggtcc 420
ggcaactgc 429

<210> 66
<211> 143
<212> PRT
<213> Cellulomonas xylanilytica

<400> 66

Arg Cys Ser Ile Gly Phe Ala Val Thr Gly Gly Phe Val Thr Ala Gly
1 5 10 15
His Cys Gly Arg Ser Gly Ala Thr Thr Thr Ser Pro Ser Gly Thr Phe
20 25 30
Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Arg Ala Ala
35 40 45
Ser Gly Asn Thr Pro Val Gly Ala Val Asn Arg Tyr Asp Gly Ser Arg
50 55 60
Val Thr Val Ala Gly Ser Thr Asp Ala Ala Val Gly Ala Ala Val Cys
65 70 75 80
Arg Ser Gly Ser Thr Thr Ala Trp Gly Cys Gly Thr Ile Gln Ser Arg
85 90 95
Gly Ala Ser Val Thr Tyr Ala Gln Gly Thr Val Ser Gly Leu Ile Arg
100 105 110
Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Ile Ala
115 120 125
Gly Thr Gln Ala Arg Gly Val Thr Ser Gly Gly Ser Gly Asn Cys
130 135 140

<210> 67
<211> 1284
<212> DNA
<213> Oerskovia turbata

<400> 67
atggcaccgat cattctggag gacgctcgcc acggcgtgcg ccgcgacggc actggttgcc 60
ggccccgcag cgctcaccgc gaacgccgcg acgcccaccc ccgacacccc gaccgtttca 120
ccccagacct cctcgaaggt ctgcggcgag gtgctccgcg ccctccagcg ggacctgggg 180

ctgagcgcca	aggacgcgac	gaagcgtctg	gcgttccagt	ccgacgcggc	gagcaccgag	240
gacgtctctg	ccgacagcct	ggacgcctac	gcggggcgct	gggtcgaccc	tgcgaggaac	300
accctgtacg	tggcgctcgc	cgacagggcc	gaggccaagg	aggctccgtt	ggccggagcg	360
acccccgtgg	tgtcgacca	cacgtctgcc	gagctcgaca	cgtggaaggc	ggcgctcgac	420
ggtgagctca	acgaccccg	gggcgtccc	agctggttcg	tcgacgtcac	gaccaaccag	480
gtcgtcgtca	acgtgcacga	cggcggacgc	gccctcgcgg	agctgggtgc	cgcgagcgcg	540
ggcgtgcccc	ccgacgccat	cacctacgtg	acgacgaccg	aggctcctcg	tcccctcgtc	600
gacgtggtgg	gcggaacgc	gtacaccatg	ggttcgggcg	ggcgctgctc	ggtcgggttc	660
gcggtgaacg	ggggcttcat	cacggccggg	cactgcggct	cggtcggcac	ccgcacctcg	720
gggcccggcg	gcacgttccg	ggggtcgaac	ttccccggca	acgactacgc	ctgggtgcag	780
gtcgacgcgg	gtaacacccc	ggtcggcgcg	gtcaacaact	acagcgggtg	gcgcgtcgcg	840
gtcgcagggt	cgacggccgc	gcccgtgggg	gcctcgggtc	gccggtccgg	ttccacgacg	900
ggctggcact	gcggcaccat	cggcgcgtac	aacacctcgg	tgacgtaccc	gcagggcacc	960
gtctcggggc	tcacccgcac	gaacgtgtgc	gccgagcccc	gcgactcggg	cggctcgtct	1020
ctcgcgggca	accaggcgca	gggcgtgacc	tggggcggtg	cgggcaactg	ctcgtcgggg	1080
gggacgacgt	acttccagcc	cgtaacagag	gccctcgggg	ggtacggggt	cacgctcgtg	1140
acctctgacg	gtggggggccc	gagccgccgc	cgaccgggtg	ccagggttat	gcgcggacct	1200
accagggcag	cgtctcggcc	gggacgtcgg	tcgcgcagcg	aacggttcgt	acgtcacgac	1260
cggggggcggg	cgaccgggtg	tgcc				1284

<210> 68
 <211> 428
 <212> PRT
 <213> Oerskovia turbata

<400> 68

Met	Ala	Arg	Ser	Phe	Trp	Arg	Thr	Leu	Ala	Thr	Ala	Cys	Ala	Ala	Thr
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Ala	Leu	Val	Ala	Gly	Pro	Ala	Ala	Leu	Thr	Ala	Asn	Ala	Ala	Thr	Pro
			20					25						30	
Thr	Pro	Asp	Thr	Pro	Thr	Val	Ser	Pro	Gln	Thr	Ser	Ser	Lys	Val	Ser
		35					40					45			
Pro	Glu	Val	Leu	Arg	Ala	Leu	Gln	Arg	Asp	Leu	Gly	Leu	Ser	Ala	Lys
	50					55					60				
Asp	Ala	Thr	Lys	Arg	Leu	Ala	Phe	Gln	Ser	Asp	Ala	Ala	Ser	Thr	Glu
65					70					75					80
Asp	Ala	Leu	Ala	Asp	Ser	Leu	Asp	Ala	Tyr	Ala	Gly	Ala	Trp	Val	Asp
				85					90					95	
Pro	Ala	Arg	Asn	Thr	Leu	Tyr	Val	Gly	Val	Ala	Asp	Arg	Ala	Glu	Ala
			100					105						110	
Lys	Glu	Val	Arg	Ser	Ala	Gly	Ala	Thr	Pro	Val	Val	Val	Asp	His	Thr
		115						120						125	
Leu	Ala	Glu	Leu	Asp	Thr	Trp	Lys	Ala	Ala	Leu	Asp	Gly	Glu	Leu	Asn
	130						135				140				
Asp	Pro	Ala	Gly	Val	Pro	Ser	Trp	Phe	Val	Asp	Val	Thr	Thr	Asn	Gln
145					150					155					160
Val	Val	Val	Asn	Val	His	Asp	Gly	Gly	Arg	Ala	Leu	Ala	Glu	Leu	Ala
				165					170					175	
Ala	Ala	Ser	Ala	Gly	Val	Pro	Ala	Asp	Ala	Ile	Thr	Tyr	Val	Thr	Thr
			180					185						190	
Thr	Glu	Ala	Pro	Arg	Pro	Leu	Val	Asp	Val	Val	Gly	Gly	Asn	Ala	Tyr
	195					200								205	
Thr	Met	Gly	Ser	Gly	Gly	Arg	Cys	Ser	Val	Gly	Phe	Ala	Val	Asn	Gly
	210					215					220				
Gly	Phe	Ile	Thr	Ala	Gly	His	Cys	Gly	Ser	Val	Gly	Thr	Arg	Thr	Ser
225					230					235					240

Gly	Pro	Gly	Gly	Thr	Phe	Arg	Gly	Ser	Asn	Phe	Pro	Gly	Asn	Asp	Tyr
				245					250					255	
Ala	Trp	Val	Gln	Val	Asp	Ala	Gly	Asn	Thr	Pro	Val	Gly	Ala	Val	Asn
			260					265					270		
Asn	Tyr	Ser	Gly	Gly	Arg	Val	Ala	Val	Ala	Gly	Ser	Thr	Ala	Ala	Pro
		275					280					285			
Val	Gly	Ala	Ser	Val	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys
	290					295					300				
Gly	Thr	Ile	Gly	Ala	Tyr	Asn	Thr	Ser	Val	Thr	Tyr	Pro	Gln	Gly	Thr
305					310					315				320	
Val	Ser	Gly	Leu	Ile	Arg	Thr	Asn	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser
			325						330					335	
Gly	Gly	Ser	Leu	Ala	Gly	Asn	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	
			340				345					350			
Gly	Ser	Gly	Asn	Cys	Ser	Ser	Gly	Gly	Thr	Thr	Tyr	Phe	Gln	Pro	Val
		355					360					365			
Asn	Glu	Ala	Leu	Gly	Gly	Tyr	Gly	Leu	Thr	Leu	Val	Thr	Ser	Asp	Gly
	370					375					380				
Gly	Gly	Pro	Ser	Arg	Arg	Arg	Pro	Gly	Ala	Arg	Ala	Met	Arg	Gly	Pro
385					390					395				400	
Thr	Arg	Ala	Ala	Ser	Arg	Pro	Gly	Arg	Arg	Ser	Arg	Ser	Glu	Arg	Phe
				405					410					415	
Val	Arg	His	Asp	Arg	Gly	Arg	Ala	Thr	Gly	Cys	Ala				
			420					425							

<210> 69
 <211> 524
 <212> DNA
 <213> Oerskovia jenensis

<400>	69	
gccgctgctc	ggtcggcttc	gcggtgaacg
cggtgggcac	ccgcacctcg	gggccgggcg
acgactacgc	ctgggtgcag	gtcgacgcgg
acagcggtag	acgcgtcgcg	gtcgcgggct
gcccgtcccg	ttccacgacg	ggctggcgct
tgacgtaccc	gcaggggacc	gtctccgggc
gcgactcggg	cggctcgcctc	ctcgcgggca
cgggcaactg	ctcgtcgggc	ggcacgacgt
cctacggcct	cacgctcgtg	acctccggcg
		gcaggggcaa
		ctgc
		60
		120
		180
		240
		300
		360
		420
		480
		524

<210> 70
 <211> 174
 <212> PRT
 <213> Oerskovia jenensis

<400>	70														
Arg	Cys	Ser	Val	Gly	Phe	Ala	Val	Asn	Gly	Gly	Phe	Val	Thr	Ala	Gly
1				5					10					15	
His	Cys	Gly	Thr	Val	Gly	Thr	Arg	Thr	Ser	Gly	Pro	Gly	Gly	Thr	Phe
			20					25					30		
Arg	Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala	Trp	Val	Gln	Val	Asp
		35					40					45			
Ala	Gly	Asn	Thr	Pro	Val	Gly	Ala	Val	Asn	Asn	Tyr	Ser	Gly	Gly	Arg
	50					55					60				
Val	Ala	Val	Ala	Gly	Ser	Thr	Ala	Ala	Pro	Val	Gly	Ser	Ser	Val	Cys

65		70		75		80									
Pro	Glu	Val	Arg	Ala	Gln	Arg	Arg	Gly	Arg	Pro	Arg	Val	Gly	Ala	Gly
				85					90					95	
Glu	Gln	Ser	Ala	Ser	Thr	Pro	Pro	Gly	Ala	His	Arg	Gly	Thr	Arg	Gly
			100					105					110		
Ala	Val	Arg	Ala	His	Gly	Asp	Val	Arg	Gly	Gly	Asp	Arg	Tyr	Ile	Thr
			115				120					125			
Arg	Asp	Pro	Gly	Ala	Ser	Ser	Gly	Ser	Ala	Cys	Ser	Ile	Gly	Tyr	Ala
			130				135					140			
Val	Gln	Gly	Gly	Phe	Val	Thr	Ala	Gly	His	Cys	Gly	Arg	Gly	Gly	Thr
				150						155					160
Arg	Arg	Val	Leu	Thr	Ala	Ser	Trp	Ala	Arg	Met	Gly	Thr	Val	Gln	Ala
				165					170						175
Ala	Ser	Phe	Pro	Gly	His	Asp	Tyr	Ala	Trp	Val	Arg	Val	Asp	Ala	Gly
			180					185					190		
Phe	Ser	Pro	Val	Pro	Arg	Val	Asn	Asn	Tyr	Ala	Gly	Gly	Thr	Val	Asp
			195				200					205			
Val	Ala	Gly	Ser	Ala	Glu	Ala	Pro	Val	Gly	Ala	Ser	Val	Cys	Arg	Ser
			210				215				220				
Gly	Ala	Thr	Thr	Gly	Trp	Arg	Cys	Gly	Val	Ile	Glu	Gln	Lys	Asn	Ile
				230						235					240
Thr	Val	Asn	Tyr	Gly	Asn	Gly	Asp	Val	Pro	Gly	Leu	Val	Arg	Gly	Ser
				245					250					255	
Ala	Cys	Ala	Glu	Gly	Gly	Asp	Ser	Gly	Gly	Ser	Val	Ile	Ser	Gly	Asn
			260					265					270		
Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Arg	Ile	Asn	Asp	Cys	Ser	Asn	Gly
			275				280					285			
Gly	Lys	Phe	Leu	Tyr	Gln	Pro	Asp	Arg	Arg	Pro	Val	Ala	Arg	Asp	His
			290			295				300					
Gly	Arg	Arg	Val	Gly	Gln	Arg	Ala	Arg	Arg	Ala	Arg	Gly	Gln	Val	His
			305		310				315					320	
Arg	Arg	Pro	Arg	Val	Arg	Leu	Gln								
				325											

<210> 73
 <211> 257
 <212> DNA
 <213> Promicromonospora citrea

<400> 73	
ttccccggca acgactacgc gtgggtgaac acggggcacgg acgacaccct cgtcggcgcc	60
gtgaacaact acagcggcgg cacggtcaac gtcgcgggct cgaccctgtc cgccgtcgcc	120
gcgacggtct gccgctcggg ctccacgacc ggctggcact gcggcaccat ccaggcgctg	180
aacgcgtcgg tcacctacgc cgagggcacc gtgagcggcc tcatccgcac caacgtgtgc	240
gccgagcccg gcgactc	257

<210> 74
 <211> 85
 <212> PRT
 <213> Promicromonospora citrea

<400> 74	
Phe Pro Gly Asn Asp Tyr Ala Trp Val Asn Thr Gly Thr Asp Asp Thr	
1 5 10 15	
Leu Val Gly Ala Val Asn Asn Tyr Ser Gly Gly Thr Val Asn Val Ala	
20 25 30	

Gly Ser Thr Arg Ala Ala Val Gly Ala Thr Val Cys Arg Ser Gly Ser
35 40 45
Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Leu Asn Ala Ser Val
50 55 60
Thr Tyr Ala Glu Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys
65 70 75 80
Ala Glu Pro Gly Asp
85

<210> 75
<211> 257
<212> DNA
<213> Promicromonospora sukumoe

<400> 75
ttccccggca acgactacgc gtgggtgaac gtcgggtccg acgacacccc gatcgggtgcg 60
gtcaacaact acagcggcgg caccgtgaac gtcgcgggct cgaccaggc cgccgtcggc 120
tccaccgtct gccgctccgg ttccacgacc ggctggcact gcggcaccat ccaggccttc 180
aacgcgtcgg tcacctacgc cgagggcacc gtgtccggcc tgatccgcac caacgtctgc 240
gccgagcccc gcgactc 257

<210> 76
<211> 85
<212> PRT
<213> Promicromonospora sukumoe

<400> 76

Phe Pro Gly Asn Asp Tyr Ala Trp Val Asn Val Gly Ser Asp Asp Thr
1 5 10 15
Pro Ile Gly Ala Val Asn Asn Tyr Ser Gly Gly Thr Val Asn Val Ala
20 25 30
Gly Ser Thr Gln Ala Ala Val Gly Ser Thr Val Cys Arg Ser Gly Ser
35 40 45
Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Phe Asn Ala Ser Val
50 55 60
Thr Tyr Ala Glu Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys
65 70 75 80
Ala Glu Pro Gly Asp
85

<210> 77
<211> 430
<212> DNA
<213> Xylanibacterium ulmi

<400> 77
gccgctgctc gatcgggttc gccgtgacgg gcggcttcgt gaccgccggc cactgcgga 60
gggtccggcg gacgacgacg tccgcgagcg gcacgttcgc cgggtccagc tttccccgca 120
acgactacgc ctgggtccgc gcggcctcgg gaacacgccg gtcggtgcgg tgaaccgcta 180
cgacggcagc cgggtgacgg tggccgggtc caccgacgcg gccgtcggtg ccgcggtctg 240
ccggtcgggg tcgacgacgg cgtggcgctg cggcacgatc cagtcccgcg gcgcgacggt 300
cacgtacgcc cagggcaccg tcagcgggct catccgcacc aacgtgtgcg ccgagccggg 360
tgactccggg gggtcgctga tcgcgggcac ccaggcgagc ggctgacgt ccggcggctc 420
cggcaactgc 430

<210> 78

<211> 141
<212> PRT
<213> Xylanibacterium ulmi

<400> 78

Arg Cys Ser Ile Gly Phe Ala Val Thr Gly Gly Phe Val Thr Ala Gly
1 5 10 15
His Cys Gly Arg Ser Gly Ala Thr Thr Thr Ser Ala Ser Gly Thr Phe
20 25 30
Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Arg Ala Ala
35 40 45
Ser Gly Asn Thr Pro Val Gly Ala Val Asn Arg Tyr Asp Gly Ser Arg
50 55 60
Val Thr Val Ala Gly Ser Thr Asp Ala Ala Val Gly Ala Ala Val Cys
65 70 75 80
Arg Ser Gly Ser Thr Thr Ala Trp Arg Cys Gly Thr Ile Gln Ser Arg
85 90 95
Gly Ala Thr Val Thr Tyr Ala Gln Gly Thr Val Ser Gly Leu Ile Arg
100 105 110
Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Ile Ala
115 120 125
Gly Thr Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly
130 135 140

<210> 79

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 79
acccacgcgt agtcgttgcc

20

<210> 80
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 80
acccacgcgt agtcgkkgcc gggg

24

<210> 81
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 81

tcgtcgtggt cgcgccgg 18

<210> 82
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 82
cgacgtgctc gcgcccg 17

<210> 83
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 83
cgcgcccagc tcgcggtg 18

<210> 84
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 84
cggccccgag gtgcgggtgc cg 22

<210> 85
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 85
cagcgtctcc ggcctcatcc gc 22

<210> 86
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 86
ctcgggtctcg ggcctcatcc gc 22

<210> 87
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 87
cgacgttccc ggctctgtgc gc

22

<210> 88
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 88
caccgtctcg gggctcatcc gc

22

<210> 89
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 89
agcargtgt gcgcgagcc

20

<210> 90
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 90
ggcagcgcgt gcgcggaggg

20

<210> 91
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 91
gccgctgctc gatcgggttc

20

<210> 92
<211> 24

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 92
 gcagttgccg gagccgccg acgt 24

 <210> 93
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 93
 tgcgccgagc ccggcgactc cggc 24

 <210> 94
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 94
 ggcacgacgt acttccagcc cgtgaac 27

 <210> 95
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 95
 gacccacgcg tagtcgttgc cggggaacga cga 33

 <210> 96
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 96
 gaaggtcccc gacggtgacg acgtgctcgc gcc 33

 <210> 97
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

 <400> 97
 caggcgagg gcgtgacctc gggcggggtcg 30

 <210> 98
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 98
 ggcgggacga cgtacttcca gcccgtcaa 29

 <210> 99
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 99
 caccacgcg tagtcgtggc cggggaacga 30

 <210> 100
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 100
 gaagccgcc tggacggcgt acccgatcga gca 33

 <210> 101
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 101
 tgcgcggagg gcggcgactc gggcggggtcg 30

 <210> 102
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> primer

<400> 102

ttcctctacc agcccgtaa cccgaccta

30

<210> 103

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 103

cgccgcgggg acgaaccgc cctcgaccgc gaa

33

<210> 104

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 104

cgcgtagtcg ttgccgggga acgacgagcc

30

<210> 105

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 105

ggcctcatcc gcacgagcgt gtgcgccgag

30

<210> 106

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 106

acgtcgggcg ggtccggcaa ctgccgctac gggggc

36

<210> 107

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 107
gagccccgtac acccggaggg cctcgttgac gggctggaa 39

<210> 108
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 108
cgtcacgccc tgcgcctggg tgcccgcgag 30

<210> 109
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 109
tccagcccggt caacgaggcc ctccgggtgt acgggctc 38

<210> 110
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 110
acgtcggtcg cgcagccgaa cggttcgtac gtc 33

<210> 111
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 111
cgtggtcgcg ccggtcgtgc cgcagtgcc 30

<210> 112
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 112
 gacgacgacc gtgttggttag tgacgtcgac gtacca 36

<210> 113
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 113
 tccaccacgg ggtggcgctg cgggacgatc 30

<210> 114
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 114
 gtgtgcgccg agcccggcga ctccggcggc 30

<210> 115
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 115
 gctcgggccc ccaccgtcag aggtcacgag cgtgag 36

<210> 116
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 116
 atggcacgat cattctggag gacgctcgcc acggcg 36

<210> 117
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 117
 tgctcgatcg ggtacgccgt ccagggcggc ttc 33

<210> 118
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 118
 taggatcggg ttgacgggct ggtagaggaa 30

 <210> 119
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 119
 tggtagctcg acgtcactac caacacgggc gtcgtc 36

 <210> 120
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 120
 gccgccggag tcgccgggct cggcgcacac 30

 <210> 121
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 121
 gtsgacgtsa tcgsgggsaa cgcstactac 30

 <210> 122
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <220>
 <221> misc_feature
 <222> (13)..(16)
 <223> n is a, c, g, or t

<400> 122
sgcsgtsgcs ggnganga

18

<210> 123
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 123
gtsgaygtsa tcggcggcga ygcstac

27

<210> 124
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<220>
<221> misc_feature
<222> (10)..(16)
<223> n is a, c, g, or t

<400> 124
sgasgcgtan ccctgncc

18

<210> 125
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> VARIANT
<222> 1, 8-16, 24, 35, 36, 38, 39, 41-44, 48, 61-64, 66, 67, 69-71, 81, 87, 89,
93, 109-111, 113, 116, 159, 160, 163-166, 169-189
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> 4, 19, 28, 108, 126
<223> Xaa is Ile or Val

<220>
<221> VARIANT
<222> 7, 157
<223> Xaa is Asn or Asp

<220>

<221> VARIANT
<222> 92, 99, 143
<223> Xaa is Ser or Ala

<220>
<221> VARIANT
<222> 112, 156
<223> Xaa is Asn or Gly

<220>
<221> VARIANT
<222> 21
<223> Xaa is Phe or Tyr

<220>
<221> VARIANT
<222> 40
<223> Xaa is Thr or Val

<220>
<221> VARIANT
<222> 59
<223> Xaa is Phe or Trp

<220>
<221> VARIANT
<222> 65
<223> Xaa is Gly or Asp

<220>
<221> VARIANT
<222> 68
<223> Xaa is Leu or Phe

<220>
<221> VARIANT
<222> 74
<223> Xaa is Asn or Arg

<220>
<221> VARIANT
<222> 75
<223> Xaa is Tyr or His

<220>
<221> VARIANT
<222> 76
<223> Xaa is Ser or Asp

<220>
<221> VARIANT
<222> 78
<223> Xaa is Gly or Ser

<220>
<221> VARIANT
<222> 79

<223> Xaa is Arg or Thr

<220>

<221> VARIANT

<222> 83

<223> Xaa is Ala or Thr

<220>

<221> VARIANT

<222> 85

<223> Xaa is His or Ser

<220>

<221> VARIANT

<222> 86

<223> Xaa is Thr or Gln

<220>

<221> VARIANT

<222> 102

<223> Xaa is Gly or Ala

<220>

<221> VARIANT

<222> 104

<223> Xaa is His or Arg

<220>

<221> VARIANT

<222> 107

<223> Xaa is Thr or Tyr

<220>

<221> VARIANT

<222> 114

<223> Xaa is Ser or Thr

<220>

<221> VARIANT

<222> 118

<223> Xaa is Pro or Ala

<220>

<221> VARIANT

<222> 119

<223> Xaa is Glu or Gln

<220>

<221> VARIANT

<222> 121

<223> Xaa is Thr, Ser, or Asp

<220>

<221> VARIANT

<222> 123

<223> Xaa is Arg or Ser

<220>
<221> VARIANT
<222> 128
<223> Xaa is Thr or Gly

<220>
<221> VARIANT
<222> 129
<223> Xaa is Thr, Asn, or Ser

<220>
<221> VARIANT
<222> 130
<223> Xaa is Val or Ala

<220>
<221> VARIANT
<222> 134
<223> Xaa is Pro or Gly

<220>
<221> VARIANT
<222> 141
<223> Xaa is Leu or Val

<220>
<221> VARIANT
<222> 142
<223> Xaa is Leu, Val, or Ile

<220>
<221> VARIANT
<222> 145
<223> Xaa is Asn or Thr

<220>
<221> VARIANT
<222> 148
<223> Xaa is Gln or Arg

<220>
<221> VARIANT
<222> 150
<223> Xaa is Val or Leu

<220>
<221> VARIANT
<222> 154
<223> Xaa is Gly or Arg

<220>
<221> VARIANT
<222> 155
<223> Xaa is Ser or Ile

<400> 125

Xaa Asp Val Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Cys Ser Xaa Gly Xaa Ala Val Xaa Gly Gly Phe Xaa Thr Ala Gly His
 20 25 30
 Cys Gly Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Thr Phe Xaa
 35 40 45
 Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Xaa Val Xaa Xaa Xaa Xaa
 50 55 60
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Asn Xaa Xaa Xaa Gly Xaa Xaa Val
 65 70 75 80
 Xaa Val Xaa Gly Xaa Xaa Xaa Ala Xaa Val Gly Xaa Xaa Val Cys Arg
 85 90 95
 Ser Gly Xaa Thr Thr Xaa Trp Xaa Cys Gly Xaa Xaa Xaa Xaa Xaa Xaa
 100 105 110
 Xaa Xaa Val Xaa Tyr Xaa Xaa Gly Xaa Val Xaa Gly Leu Xaa Arg Xaa
 115 120 125
 Xaa Xaa Cys Ala Glu Xaa Gly Asp Ser Gly Gly Ser Xaa Xaa Xaa Gly
 130 135 140
 Xaa Gln Ala Xaa Gly Xaa Thr Ser Gly Xaa Xaa Xaa Xaa Cys Xaa Xaa
 145 150 155 160
 Gly Gly Xaa Xaa Xaa Xaa Gln Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 165 170 175
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 180 185

<210> 126
 <211> 16
 <212> PRT
 <213> Cellulomonas cellasea

<220>
 <221> VARIANT
 <222> (1)..(1)
 <223> Xaa is Ile or Tyr

<400> 126

Xaa Ala Trp Asp Ala Phe Ala Glu Asn Val Val Asp Trp Ser Ser Arg
 1 5 10 15

<210> 127
 <211> 17
 <212> PRT
 <213> Cellulomonas cellasea

<400> 127

Tyr Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ile Leu Gln Ala
 1 5 10 15
 Tyr

<210> 128
 <211> 11
 <212> PRT
 <213> Cellulomonas flavigena

<220>
 <221> VARIANT
 <222> (4)..(11)
 <223> Xaa is Ile or Tyr

<400> 128

Val Asp Val Xaa Gly Gly Asn Ala Tyr Tyr Xaa
 1 5 10

<210> 129
 <211> 9
 <212> PRT
 <213> Cellulomonas fimi

<220>
 <221> VARIANT
 <222> (4)..(4)
 <223> Xaa is Ile or Tyr

<400> 129

Val Asp Val Xaa Gly Gly Asp Ala Tyr
 1 5

<210> 130
 <211> 305
 <212> DNA
 <213> Aspergillus niger

<220>
 <221> misc_feature
 <222> (186)..(186)
 <223> n is a, c, g, or t

<400> 130
 tcgaacttca tgttcgagtt cttgttcacg tagaagccgg agatgtgaga ggtgatctgg 60
 aactgctcac cctcggttgg ggtgacctgg aggtaaagca agtgaccctt ctggcggagg 120
 tggttaaggaa cgggggttcca cggggagaga gagatggcct tgacgggtctt gggaagggga 180
 gcttcngcgc gggggaggat ggtcttgaga gagggggagc tagtaatgtc gtacttggac 240
 agggagtgtc ctttctccga cgcacagcc acctcagcgg agatggcatc gtgcagagac 300
 agacc 305

<210> 131
 <211> 1488
 <212> DNA
 <213> Cellulomonas strain 69B4

<400> 131
 atgacaccac gaactgtcac aagagctctg gctgtggcaa cagcagctgc tacactcttg 60
 gctgggggta tggcagcaca agctaacgaa cgggtcctc caggatctgc atcagcccct 120
 ccacgattag ctgaaaaact tgacctgac ttacttgaag caatggaacg cgatctgggg 180
 ttagatgcag aggaagcagc tgcaacgtta gcttttcagc atgacgcagc tgaaacggga 240
 gaggctcttg ctgaggaact cgacgaagat ttcgcgggca cgtgggttga agatgatgtg 300
 ctgtatggtg caaccactga tgaagatgct gttgaagaag tcgaaggcga aggagcaact 360
 gctgtgactg ttgagcattc tcttgctgat ttagaggcgt ggaagacggt tttggatgct 420
 gcgctggagg gtcattgatga tgtgcctacg tggtacgtcg acgtgcctac gaattcggta 480

gtcgttgctg	taaaggcagg	agcgcaggat	gtagctgcag	gacttgtgga	aggcgctgat	540
gtgccatcag	atgcggtcac	ttttgtagaa	acggacgaaa	cgcctagaac	gatgttcgac	600
gtaattggag	gcaacgcata	tactattggc	ggccggtcta	gatgttctat	cggattcgca	660
gtaaacgggtg	gcttcattac	tgccggtcac	tgcggaagaa	caggagccac	tactgccaat	720
ccgactggca	catttgcagg	tagctcgttt	ccgggaaatg	attatgcatt	cgtccgaaca	780
ggggcaggag	taaatttgct	tgccccagtc	aataactact	cgggcggcag	agtccaagta	840
gcaggacata	cggccgcacc	agttggatct	gctgtatgcc	gctcaggtag	cactacaggt	900
tggcattgcg	gaactatcac	ggcgctgaat	tcgtctgtca	cgtatccaga	gggaacagtc	960
cgaggactta	tccgcacgac	ggtttgtgcc	gaaccagggtg	atagcggagg	tagcctttta	1020
gcgggaaatc	aagcccaagg	tgtaacgtca	ggtggttctg	gaaattgtcg	gacgggggga	1080
acaacattct	ttcaaccagt	caacccgatt	ttgcaggctt	acggcctgag	aatgattacg	1140
actgactctg	gaagttcccc	tgtccagca	cctacatcat	gtacaggcta	cgcaagaacg	1200
ttcacaggaa	ccctcgcagc	aggaagagca	gcagctcaac	cgaacggtag	ctatgttcag	1260
gtcaaccgga	gcggtacaca	ttccgtctgt	ctcaatggac	ctagcgggtc	ggactttgat	1320
ttgtatgtgc	agcgatggaa	tggcagtagc	tgggtaaccg	tcgctcaatc	gacatcgccg	1380
ggaagcaatg	aaaccattac	gtaccgcgga	aatgctggat	attatcgcta	cgtggttaac	1440
gctgcgtcag	gatcaggagc	ttacacaatg	ggactcaccc	tcccctga		1488

<210> 132

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 132

Asp Asp Asn Asp Pro Ile

1 5

<210> 133

<211> 1020

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 133

gtgagaagca	aaaaattgtg	gatcagcttg	ttgtttgcgt	taacgttaat	ctttacgatg	60
gcgttcagca	acatgagcgc	gcaggctgat	gattattcag	ttgtagagga	acatgggcaa	120
ctaagtatta	gtaacgggtga	attagtcaat	gaacgaggcg	aacaagttca	gttaaaaggg	180
atgagttccc	atggtttgca	atggtacggt	caatttgtaa	actatgaaag	catgaaatgg	240
ctaagagatg	attgggggaat	aactgtattc	cgagcagcaa	tgtatacctc	ttcaggagga	300
tatattgacg	atccatcagt	aaaggaaaaa	gtaaaagaga	ctgttgaggc	tgcgatagac	360
cttggcatat	atgtgatcat	tgattggcat	atcctttcag	acaatgaccc	gaatataatat	420
aaagaagaag	cgaaggattt	ctttgatgaa	atgtcagagt	tgtatggaga	ctatccgaat	480
gtgatatacg	aaattgcaaa	tgaaccgaat	ggtagtgatg	ttacgtggga	caatcaaata	540
aaaccgtatg	cagaagaagt	gattccgggt	attcgtgaca	atgaccctaa	taacattggt	600
attgtaggta	caggtagcatg	gagtcaggat	gtccatcatg	cagccgataa	tcagcttgca	660
gacctaacg	tcattgtatgc	atttcatttt	tatgcaggaa	cacatggaca	aaattttacga	720
gaccaagtag	attatgcatt	agatcaagga	gcagcgatat	ttgttagtga	atgggggaca	780
agtgcagcta	caggtgatgg	tggtgtgttt	ttagatgaag	cacaagtgtg	gattgacttt	840
atggatgaaa	gaaatttaag	ctggggccaac	gggtctctaa	cgcataagga	tgagtcatct	900
gcagcggttaa	tgccagggtg	aaatccaact	gggtggttga	cagaggctga	actatctcca	960
tctggtacat	ttgtgaggga	aaaaataaga	gaatcagcat	ctgacaacaa	tgatcccata	1020

<210> 134
 <211> 340
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 134

Val Arg Ser Lys Lys Leu Trp Ile Ser Leu Leu Phe Ala Leu Thr Leu
 1 5 10 15
 Ile Phe Thr Met Ala Phe Ser Asn Met Ser Ala Gln Ala Asp Asp Tyr
 20 25 30
 Ser Val Val Glu Glu His Gly Gln Leu Ser Ile Ser Asn Gly Glu Leu
 35 40 45
 Val Asn Glu Arg Gly Glu Gln Val Gln Leu Lys Gly Met Ser Ser His

50 55 60
 Gly Leu Gln Trp Tyr Gly Gln Phe Val Asn Tyr Glu Ser Met Lys Trp
 65 70 75 80
 Leu Arg Asp Asp Trp Gly Ile Thr Val Phe Arg Ala Ala Met Tyr Thr
 85 90 95
 Ser Ser Gly Gly Tyr Ile Asp Asp Pro Ser Val Lys Glu Lys Val Lys
 100 105 110
 Glu Thr Val Glu Ala Ala Ile Asp Leu Gly Ile Tyr Val Ile Ile Asp
 115 120 125
 Trp His Ile Leu Ser Asp Asn Asp Pro Asn Ile Tyr Lys Glu Glu Ala
 130 135 140
 Lys Asp Phe Phe Asp Glu Met Ser Glu Leu Tyr Gly Asp Tyr Pro Asn
 145 150 155 160
 Val Ile Tyr Glu Ile Ala Asn Glu Pro Asn Gly Ser Asp Val Thr Trp
 165 170 175
 Asp Asn Gln Ile Lys Pro Tyr Ala Glu Glu Val Ile Pro Val Ile Arg
 180 185 190
 Asp Asn Asp Pro Asn Asn Ile Val Ile Val Gly Thr Gly Thr Trp Ser
 195 200 205
 Gln Asp Val His His Ala Ala Asp Asn Gln Leu Ala Asp Pro Asn Val
 210 215 220
 Met Tyr Ala Phe His Phe Tyr Ala Gly Thr His Gly Gln Asn Leu Arg
 225 230 235 240
 Asp Gln Val Asp Tyr Ala Leu Asp Gln Gly Ala Ala Ile Phe Val Ser
 245 250 255
 Glu Trp Gly Thr Ser Ala Ala Thr Gly Asp Gly Gly Val Phe Leu Asp
 260 265 270
 Glu Ala Gln Val Trp Ile Asp Phe Met Asp Glu Arg Asn Leu Ser Trp
 275 280 285
 Ala Asn Trp Ser Leu Thr His Lys Asp Glu Ser Ser Ala Ala Leu Met
 290 295 300
 Pro Gly Ala Asn Pro Thr Gly Gly Trp Thr Glu Ala Glu Leu Ser Pro
 305 310 315 320
 Ser Gly Thr Phe Val Arg Glu Lys Ile Arg Glu Ser Ala Ser Asp Asn
 325 330 335
 Asn Asp Pro Ile
 340

<210> 135
<211> 30
<212> PRT
<213> Cellulomonas strain 69B4

<400> 135

Met	Arg	Ser	Lys	Lys	Arg	Thr	Val	Thr	Arg	Ala	Leu	Ala	Val	Ala	Thr
1			5					10					15		
Ala	Ala	Ala	Thr	Leu	Leu	Ala	Gly	Gly	Met	Ala	Ala	Gln	Ala		
			20					25					30		

<210> 136
<211> 30
<212> PRT
<213> Cellulomonas strain 69B4

<400> 136

Met	Arg	Ser	Lys	Lys	Leu	Trp	Ile	Ser	Leu	Leu	Leu	Ala	Val	Ala	Thr
1			5					10					15		
Ala	Ala	Ala	Thr	Leu	Leu	Ala	Gly	Gly	Met	Ala	Ala	Gln	Ala		
			20					25					30		

<210> 137
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 137
ctagctaggt accatgacac cacgaactgt cacaagagct

40

<210> 138
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 138
gtgtgcaagc tttcagggga gggtagtcc cattgtgtaa

40

<210> 139
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 139
ctagctaggt accatgacac cacgaactgt cacaagagct

40

<210> 140
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 140
gtgtgcaagc tttcaagggg aacttccaga gtcagtc

37

<210> 141
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 141
tcatgcaggg taccatgaga agcaagaagc gaactgtcac aagagctctg gct

53

<210> 142
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 142
gtgtgcaagc tttcagggga gggtagtcc cattgtgtaa

40

<210> 143
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 143
tcatgcaggg taccatgaga agcaagaagc gaactgtcac aagagctctg gct

53

<210> 144
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 144
gtgtgcaagc tttcaagggg aacttccaga gtcagtc

37

<210> 145

<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 145
tcatgcaggg taccatgaga agcaagaagt tgtggatcag ttgctgctg gctgtggcaa 60
cagcagctgc taca 74

<210> 146
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 146
gtgtgcaagc tttcagggga gggtagtcc catttgttaa 40

<210> 147
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 147
tcatgcaggg taccatgaga agcaagaagt tgtggatcag ttgctgctg gctgtggcaa 60
cagcagctgc taca 74

<210> 148
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 148
gtgtgcaagc tttcaagggg aacttccaga gtcagtc 37

<210> 149
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 149

ccataccgga tccaaacgaa cgggtcctc caggatct 38

<210> 150

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 150

ctcgagttaa gcttttaagg ggaacttcca gagtcagtc 39

<210> 151

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 151

tgagctgcta gcaaaaggag agggtaaaga atgacaccac gaactgtc 48

<210> 152

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 152

cgtacatccc gggtcagggg agggtgagtc ccattg 36

<210> 153

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 153

tgagctgcta gcaaaaggag agggtaaaga atgacaccac gaactgtc 48

<210> 154

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 154

catgcatccc ggggttaaggg gaacttccag agtcagtc 38

<210> 155
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 155
 tgagctgcta gcaaaaggag agggtaaaga atgagaagca agaag 45

 <210> 156
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 156
 cgtacatccc gggtcagggg agggtgagtc ccattg 36

 <210> 157
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 157
 tgagctgcta gcaaaaggag agggtaaaga atgagaagca agaag 45

 <210> 158
 <211> 38

 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 158
 catgcatccc gggttaaggg gaacttccag agtcagtc 38

 <210> 159
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 159
 tgagctgcta gcaaaaggag agggtaaaga atgagaagca agaag 45

<210> 160
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 160
cgtacatccc gggtcagggg agggtagtc ccattg 36

<210> 161
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 161
tgagctgcta gcaaaaggag agggtaaaga atgagaagca agaag 45

<210> 162
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 162
catgcatccc gggttaaggg gaacttccag agtcagtc 38

<210> 163
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 163
tgcagtctgc tagcaaaagg agagggtaaa gagtgagaag 40

<210> 164
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 164
catgcatccc gggttaaggg gaacttccag agtcagtc 38

<210> 165
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 165
ttatgcgagg ctagcaaaag gagagggtaa agagtgagaa gcaaaaaacg

50

<210> 166
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 166
taaagagtga gaagcaaaaa acgcacagtc acgcggggccc tg

42

<210> 167
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 167
gtcctctgtt aacttacggg ctgctgcccc agtcc

35

<210> 168
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 168
gcaacatgtc tgcgcaggct aacgaaccgg ctctccagg a

41

<210> 169
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 169
gacatgacat aagcttaagg ggaacttcca gagtc

35

<210> 170
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 170
gagccgaatt catatacctg ccggt

25

<210> 171
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 171
tcctggagga gccggttcgt tagcctgcgc agacatgttg c

41

<210> 172
<211> 5713
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 172
catcacatat acctgccgtt cactattatt tagtgaaatg agatattatg atatcttctg 60
aattgtgatt aaaaaggcaa ctttatgccc atgcaacaga aactataaaa aatacagaga 120
atgaaaagaa acagatagat ttttttagttc tttaggcccc tagtctgcaa atccttttat 180
gattttctat caaacaaaag aggaaaatag accagttgca atccaaacga gagtctaata 240
gaatgaggtc acagaatagt cttttaagta agtctactct gaattttttt aaaaggagag 300
ggtaaagagt gagaagcaaa aaattgtgga tcagcttggt gtttgcgta acgttaatct 360
ttacgatggc gttcagcaac atgtctgcgc aggctaacga accggctcct ccaggatctg 420
catcagcccc tccacgatta gctgaaaaac ttgacctga cttacttgaa gcaatggaac 480
gcatctcggg gttagatgca gaggaagcag ctgcaacgtt agcttttcag catgacgcag 540
ctgaaacggg agaggctctt gctgaggaac tgcacgaaga tttcgcgggc acgtgggttg 600
aagatgatgt gctgtatgtt gcaaccactg atgaagatgc tgttgaagaa gtcgaaggcg 660
aaggagcaac tgctgtgact gttgagcatt ctcttgctga tttagaggcg tggaagacgg 720
ttttggatgc tgcgctggag ggtcatgatg atgtgcctac gtggtacgtc gacgtgccta 780
cgaattcggg agtcgttgct gtaaaggcag gacgcagga tgtagctgca ggacttgtgg 840
aaggcgctga tgtgccatca gatgcggtca cttttgtaga aacggacgaa acgcctagaa 900
cgatgttcga cgtaattgga ggcaacgcat atactattgg cggccggtct agatgttcta 960
tcggattcgc agtaaacggt ggcttcatta ctgccggtca ctgcggaaga acaggagcca 1020
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Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala Asn Glu Pro Ala
          20          25          30
Pro

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<210> 174
<211> 36
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<220>
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          20          25          30
Glu Pro Ala Pro
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acaaaaacgg ctttac 136

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ggatct 66

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ggatct 66

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<400> 213
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<213> Cellulomonas strain 69B4

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			20				25					30			
Pro	Ala	Pro	Pro	Gly	Ser	Ala	Ser	Ala	Pro	Pro	Arg	Leu	Ala	Glu	Lys
			35				40					45			
Leu	Asp	Pro	Asp	Leu	Leu	Glu	Ala	Met	Glu	Arg	Asp	Leu	Gly	Leu	Asp
	50					55					60				
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65					70				75					80	
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 Val Glu Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val Glu His
 115 120 125
 Ser Leu Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala Ala Leu
 130 135 140
 Glu Gly His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro Thr Asn
 145 150 155 160
 Ser Val Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala Ala Gly
 165 170 175
 Leu Val Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe Val Glu
 180 185 190
 Thr Asp Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly Asn Ala
 195 200 205
 Tyr Thr Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala Val Asn
 210 215 220
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 225 230 235 240
 Ala Asn Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp
 245 250 255
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 Cys Gly Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro Glu Gly
 305 310 315 320
 Thr Val Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly Asp
 325 330 335
 Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser
 340 345 350
 Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe Gln Pro
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<223> n is a, c, g, or t

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<400> 262
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<210> 265
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<400> 265
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<210> 266
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 <210> 302
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 <400> 303
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 <400> 304

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<210> 305

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<400> 305

gcaggacata cggccgcann sgttggatct gctgtatgc

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<210> 306

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<400> 306

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<400> 315
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<400> 321
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39

<210> 322
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<400> 322
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<210> 323

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<400> 323
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<210> 326

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<400> 327
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<210> 328
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<400> 328
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<210> 329
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<400> 329
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<210> 331
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<400> 331
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<400> 332
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<210> 333
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<400> 333

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<210> 334

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<220>

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<223> n is a, c, g, or t

<400> 334

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<210> 335

<211> 39

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<223> n is a, c, g, or t

<400> 335

tcgtctgtca cgtatccann sggaacagtc cgaggactt

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<210> 336

<211> 39

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<223> primer

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<400> 336
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<400> 337
gtcacgtatc cagagggann sgtccgagga cttatccgc

39

<210> 338
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<400> 338
acgtatccag agggaacann scgaggactt atccgcacg

39

<210> 339
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<400> 339
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39

<210> 340
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<400> 340
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<210> 341
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<400> 341
gaggggaacag tccgaggann satccgcacg acggtttgt

39

<210> 342
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<400> 342
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<210> 343
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<400> 343

acagtccgag gacttatacnn sacgacgggtt tgtgccgaa

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<210> 344

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<400> 344

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<400> 345

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39

<210> 346

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<210> 347

<211> 39

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<400> 347

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<210> 348

<211> 39

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<400> 348

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<210> 349

<211> 39

<212> DNA

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<210> 350

<211> 39

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<210> 351

<211> 39

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<210> 352

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<400> 352

gtttgtgccg aaccaggtnn sagcggaggt agcctttta

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<210> 353

<211> 39

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<220>

<221> misc_feature

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<400> 353

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<210> 354

<211> 39

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<220>

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<400> 354
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39

<210> 355
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<400> 355
gaaccagggtg atagcggann sagcctttta gcgggaaat

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<210> 356
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<223> n is a, c, g, or t

<400> 356
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<210> 357
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<400> 357
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39

<210> 358
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<210> 363

<211> 39
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<400> 363
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<210> 364
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<400> 364

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<210> 365

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<222> (19)..(20)

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<400> 365

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<210> 366

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<222> (19)..(20)

<223> n is a, c, g, or t

<400> 366

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<210> 367

<211> 39

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<223> n is a, c, g, or t

<400> 367

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39

<210> 368

<211> 39

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<213> Artificial Sequence

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<400> 368
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39

<210> 369
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<400> 369
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39

<210> 370
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<210> 371
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<400> 371
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<210> 372
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<400> 372
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<210> 373
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<223> n is a, c, g, or t

<400> 373
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<210> 374
<211> 39
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<223> n is a, c, g, or t

<400> 374
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39

<210> 375
<211> 39
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<223> n is a, c, g, or t

<400> 375
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39

<210> 376
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<400> 376
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<400> 529
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<400> 530
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<210> 559

<211> 39

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<210> 560

<211> 39

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<222> (20)..(21)

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39

<210> 561

<211> 39

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<220>

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<400> 561

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<210> 562
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<210> 563
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<400> 563
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<210> 564
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<400> 564
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<400> 565
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39

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<210> 568
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<400> 568
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<400> 571
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<210> 572
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<222> (20)..(21)

<223> n is a, c, g, or t

<400> 572

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<210> 573

<211> 39

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<222> (20)..(21)

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<400> 573

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<210> 574

<211> 39

<212> DNA

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<210> 575

<211> 39

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<400> 575

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<210> 576

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<210> 577
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<210> 578
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<400> 578
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<400> 579
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<210> 580
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<400> 580
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<210> 581
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<223> n is a, c, g, or t

<400> 581
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<210> 582
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<400> 582
agtcgtaatc attctcagsn ngtaagcctg caaaatcgg

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<210> 583
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<212> DNA
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<223> n is a, c, g, or t

<400> 583
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<210> 584
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<400> 584
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39

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<400> 590
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39

<210> 591
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<400> 591
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39

<210> 592
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<400> 592
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39

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39

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<400> 594
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39

<210> 595
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<212> DNA
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<400> 595
gcatatacta ttggcggcct gtctagatgt tctatcggg

39

<210> 596
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<220>
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<400> 596
actattggcg gccggtctca gtgttctatc ggattcgc

38

<210> 597
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<400> 597
ctgccggtca ctgccgattt acaggagcca ctactgc

37

<210> 598

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 <400> 598
 atgattatgc attcgtctca acaggggcag gagtaaat 38

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 <400> 599
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 <210> 600
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 <220>
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 <400> 600
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 <210> 601
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 <400> 601
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 <210> 602
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 <400> 602
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<211> 37
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<400> 603
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37

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<400> 604
ttggcggccg gtctagatca tctatcggat tcgcagta

38

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<400> 605
tcattactgc cggtcactca ggaagaacag gagccact

38

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<400> 606
cagttggatc tgctgtatct cgctcaggta gcactac

37

<210> 607
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<400> 607
cactacaggt tggcattcag gaactatcac ggcgctg

37

<210> 608
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<213> Artificial Sequence

<220>

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<400> 608

cttatccgca cgacggtttc agccgaacca ggtgatag

38

<210> 609

<211> 37

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<400> 609

caggtgggttc tggaaattca cggacggggg gaacaac

37

<210> 610

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 610

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19

<210> 611

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 611

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19

<210> 612

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 612

ctcggttatg agttagttc

19

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<211> 50

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<213> Artificial Sequence

<220>
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 614
 gcgtcctcca gaatgatcgt gccatgggta cctccggggg tctgtctctg 50

<210> 615
 <211> 55
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 615
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<210> 616
 <211> 42
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<220>
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<400> 616
 gcagcctgaa ctagttgcga tcctctagag atcgaacttc at 42

<210> 617
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 617
 agaccgacga gaccccgagg accatggctc acgtcatcgg cggcaacgcg tactac 56

<210> 618
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 618
tcagccgatac cgctcgcgga tccccattgt cagcccagga cgagacgcag accgta 56

<210> 619
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 619
gtagtacgcg ttgccgccga tgacgtcgac catggtccgc ggggtctcgt cggctc 56

<210> 620
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 620
gcagcctgaa ctagttgcga tcctctagag atcgaacttc atgttcga 48

<210> 621
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 621
accgacgaga ccccgccggac catgcacggc gacgtgcgcg gcggcgaccg cta 53

<210> 622
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 622
tagcggtcgc cgccgcgcac gtcgccgtgc atggtccgcg ggggtctcgtc ggt 53

<210> 623
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 623

tcagccgata cgctcgcgga tccccattgt cagcgagccc gacgagcgcg ctgcccgcac

59

<210> 624

<211> 184

<212> PRT

<213> Cellulomonas strain 69B4

<400> 624

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Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg
1      5      10      15
Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His
      20      25      30
Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala
      35      40      45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala
      50      55      60
Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val
      65      70      75      80
Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg
      85      90      95
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn
      100     105     110
Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr
      115     120     125
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly
      130     135     140
Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
      145     150     155     160
Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr
      165     170     175
Gly Leu Arg Met Ile Thr Thr Asp
      180

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<210> 625

<211> 187

<212> PRT

<213> Streptomyces griseus

<400> 625

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Val Leu Gly Gly Gly Ala Ile Tyr Gly Gly Gly Ser Arg Cys Ser Ala
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Ala Phe Asn Val Thr Lys Gly Gly Ala Arg Tyr Phe Val Thr Ala Gly
      20      25      30
His Cys Thr Asn Ile Ser Ala Asn Trp Ser Ala Ser Ser Gly Gly Ser
      35      40      45
Val Val Gly Val Arg Glu Gly Thr Ser Phe Pro Thr Asn Asp Tyr Gly
      50      55      60
Ile Val Arg Tyr Thr Asp Gly Ser Ser Pro Ala Gly Thr Val Asp Leu
      65      70      75      80
Tyr Asn Gly Ser Thr Gln Asp Ile Ser Ser Ala Ala Asn Ala Val Val
      85      90      95
Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val Thr Ser Gly
      100     105     110
Thr Val Thr Ala Val Asn Val Thr Val Asn Tyr Gly Asp Gly Pro Val
      115     120     125

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Tyr	Asn	Met	Val	Arg	Thr	Thr	Ala	Cys	Ser	Ala	Gly	Gly	Asp	Ser	Gly
130						135					140				
Gly	Ala	His	Phe	Ala	Gly	Ser	Val	Ala	Leu	Gly	Ile	His	Ser	Gly	Ser
145					150					155					160
Ser	Gly	Cys	Ser	Gly	Thr	Ala	Gly	Ser	Ala	Ile	His	Gln	Pro	Val	Thr
				165					170					175	
Glu	Ala	Leu	Ser	Ala	Tyr	Gly	Val	Thr	Val	Tyr					
			180					185							

<210> 626
 <211> 185
 <212> PRT
 <213> Streptomyces griseus

<400> 626

Ile	Ser	Gly	Gly	Asp	Ala	Ile	Tyr	Ser	Ser	Thr	Gly	Arg	Cys	Ser	Leu
1				5					10					15	
Gly	Phe	Asn	Val	Arg	Ser	Gly	Ser	Thr	Tyr	Tyr	Phe	Leu	Thr	Ala	Gly
			20					25					30		
His	Cys	Thr	Asp	Gly	Ala	Thr	Thr	Trp	Trp	Ala	Asn	Ser	Ala	Arg	Thr
		35					40					45			
Thr	Val	Leu	Gly	Thr	Thr	Ser	Gly	Ser	Ser	Phe	Pro	Asn	Asn	Asp	Tyr
		50				55					60				
Gly	Ile	Val	Arg	Tyr	Thr	Asn	Thr	Thr	Ile	Pro	Lys	Asp	Gly	Thr	Val
65					70					75					80
Gly	Gly	Gln	Asp	Ile	Thr	Ser	Ala	Ala	Asn	Ala	Thr	Val	Gly	Met	Ala
				85					90					95	
Val	Thr	Arg	Arg	Gly	Ser	Thr	Thr	Gly	Thr	His	Ser	Gly	Ser	Val	Thr
			100					105					110		
Ala	Leu	Asn	Ala	Thr	Val	Asn	Tyr	Gly	Gly	Gly	Asp	Val	Val	Tyr	Gly
			115					120					125		

Met	Ile	Arg	Thr	Asn	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	Gly	Pro
130						135					140				
Leu	Tyr	Ser	Gly	Thr	Arg	Ala	Ile	Gly	Leu	Thr	Ser	Gly	Gly	Ser	Gly
145					150					155					160
Asn	Cys	Ser	Ser	Gly	Gly	Thr	Thr	Phe	Phe	Gln	Pro	Val	Thr	Glu	Ala
				165					170					175	
Leu	Val	Ala	Tyr	Gly	Val	Ser	Val	Tyr							
			180					185							

<210> 627
 <211> 198
 <212> PRT
 <213> Lysobacter enzymogenes

<400> 627

Ala	Asn	Ile	Val	Gly	Gly	Ile	Glu	Tyr	Ser	Ile	Asn	Asn	Ala	Ser	Leu
1				5					10					15	
Cys	Ser	Val	Gly	Phe	Ser	Val	Thr	Arg	Gly	Ala	Thr	Lys	Gly	Phe	Val
			20					25					30		
Thr	Ala	Gly	His	Cys	Gly	Thr	Val	Asn	Ala	Thr	Ala	Arg	Ile	Gly	Gly
			35				40					45			

Ala	Val	Val	Gly	Thr	Phe	Ala	Ala	Arg	Val	Phe	Pro	Gly	Asn	Asp	Arg
50						55				60					
Ala	Trp	Val	Ser	Leu	Thr	Ser	Ala	Gln	Thr	Leu	Leu	Pro	Arg	Val	Ala
65						70				75					80
Asn	Gly	Ser	Ser	Phe	Val	Thr	Val	Arg	Gly	Ser	Thr	Glu	Ala	Ala	Val
				85					90					95	
Gly	Ala	Ala	Val	Cys	Arg	Ser	Gly	Arg	Thr	Thr	Gly	Tyr	Gln	Cys	Gly
			100					105					110		
Thr	Ile	Thr	Ala	Lys	Asn	Val	Thr	Ala	Asn	Tyr	Ala	Glu	Gly	Ala	Val
		115					120					125			
Arg	Gly	Leu	Thr	Gln	Gly	Asn	Ala	Cys	Met	Gly	Arg	Gly	Asp	Ser	Gly
	130					135					140				
Gly	Ser	Trp	Ile	Thr	Ser	Ala	Gly	Gln	Ala	Gln	Gly	Val	Met	Ser	Gly
145					150					155					160
Gly	Asn	Val	Gln	Ser	Asn	Gly	Asn	Asn	Cys	Gly	Ile	Pro	Ala	Ser	Gln
			165						170					175	
Arg	Ser	Ser	Leu	Phe	Glu	Arg	Leu	Gln	Pro	Ile	Leu	Ser	Gln	Tyr	Gly
			180					185					190		
Leu	Ser	Leu	Val	Thr	Gly										
			195												

<210> 628
 <211> 191
 <212> PRT
 <213> Streptomyces fradiae

<400> 628

Ile	Ala	Gly	Gly	Glu	Ala	Ile	Tyr	Ala	Ala	Gly	Gly	Gly	Arg	Cys	Ser
1				5					10					15	
Leu	Gly	Phe	Asn	Val	Arg	Ser	Ser	Ser	Gly	Ala	Thr	Tyr	Ala	Leu	Thr
			20					25					30		
Ala	Gly	His	Cys	Thr	Glu	Ile	Ala	Ser	Thr	Trp	Tyr	Thr	Asn	Ser	Gly
		35					40					45			
Gln	Thr	Ser	Leu	Leu	Gly	Thr	Arg	Ala	Gly	Thr	Ser	Phe	Pro	Gly	Asn
	50					55					60				
Asp	Tyr	Gly	Leu	Ile	Arg	His	Ser	Asn	Ala	Ser	Ala	Ala	Asp	Gly	Arg
65					70					75					80
Val	Tyr	Leu	Tyr	Asn	Gly	Ser	Tyr	Arg	Asp	Ile	Thr	Gly	Ala	Gly	Asn
				85					90					95	
Ala	Tyr	Val	Gly	Gln	Thr	Val	Gln	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Leu
			100					105					110		
His	Ser	Gly	Arg	Val	Thr	Gly	Leu	Asn	Ala	Thr	Val	Asn	Tyr	Gly	Gly
		115					120					125			
Gly	Asp	Ile	Val	Ser	Gly	Leu	Ile	Gln	Thr	Asn	Val	Cys	Ala	Glu	Pro
	130					135					140				
Gly	Asp	Ser	Gly	Gly	Ala	Leu	Phe	Ala	Gly	Ser	Thr	Ala	Leu	Gly	Leu
145					150					155					160
Thr	Ser	Gly	Gly	Ser	Gly	Asn	Cys	Arg	Thr	Gly	Gly	Thr	Thr	Phe	Phe
				165					170					175	
Gln	Pro	Val	Thr	Glu	Ala	Leu	Ser	Ala	Tyr	Gly	Val	Ser	Ile	Leu	
			180					185					190		

<210> 629
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 <212> PRT
 <213> Streptomyces griseus

<400> 629

Ile Ala Gly Gly Glu Ala Ile Thr Thr Gly Gly Ser Arg Cys Ser Leu
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Gly Phe Asn Val Ser Val Asn Gly Val Ala His Ala Leu Thr Ala Gly
20 25 30
His Cys Thr Asn Ile Ser Ala Ser Trp Ser Ile Gly Thr Arg Thr Gly
35 40 45
Thr Ser Phe Pro Asn Asn Asp Tyr Gly Ile Ile Arg His Ser Asn Pro
50 55 60
Ala Ala Ala Asp Gly Arg Val Tyr Leu Tyr Asn Gly Ser Tyr Gln Asp
65 70 75 80
Ile Thr Thr Ala Gly Asn Ala Phe Val Gly Gln Ala Val Gln Arg Ser
85 90 95
Gly Ser Thr Thr Gly Leu Arg Ser Gly Ser Val Thr Gly Leu Asn Ala
100 105 110
Thr Val Asn Tyr Gly Ser Ser Gly Ile Val Tyr Gly Met Ile Gln Thr
115 120 125
Asn Val Cys Ala Gln Pro Gly Asp Ser Gly Gly Ser Leu Phe Ala Gly
130 135 140
Ser Thr Ala Leu Gly Leu Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
145 150 155 160
Gly Gly Thr Thr Phe Tyr Gln Pro Val Thr Glu Ala Leu Ser Ala Tyr
165 170 175
Gly Ala Thr Val Leu
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<210> 630

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 630

Pro Arg Thr Met Phe Asp
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<210> 631

<211> 10

<212> PRT

<213> Cellulomonas strain 69B4

<400> 631

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr
1 5 10

<210> 632

<211> 9

<212> PRT

<213> Cellulomonas strain 69B4

<400> 632

Thr Ala Asn Pro Thr Gly Thr Phe Ala
1 5

<210> 633
<211> 12
<212> PRT
<213> Cellulomonas strain 69B4

<400> 633

Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala
1 5 10

<210> 634
<211> 14
<212> PRT
<213> Cellulomonas strain 69B4

<400> 634

Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val
1 5 10

<210> 635
<211> 10
<212> PRT
<213> Cellulomonas strain 69B4

<400> 635

Arg Thr Gly Ala Gly Val Asn Leu Leu Ala
1 5 10

<210> 636
<211> 9
<212> PRT
<213> Cellulomonas strain 69B4

<400> 636

Phe Phe Gln Pro Val Asn Pro Ile Leu
1 5

<210> 637

<211> 11
<212> PRT
<213> Cellulomonas strain 69B4

<400> 637

Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala
1 5 10

<210> 638

<211> 13
 <212> PRT
 <213> Cellulomonas strain 69B4

<400> 638

Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr Gly
 1 5 10

<210> 639
 <211> 255
 <212> PRT
 <213> Streptogrisin C

<400> 639

Ala Asp Ile Arg Gly Gly Asp Ala Tyr Tyr Met Asn Gly Ser Gly Arg
 1 5 10 15
 Cys Ser Val Gly Phe Ser Val Thr Arg Gly Thr Gln Asn Gly Phe Ala
 20 25 30
 Thr Ala Gly His Cys Gly Arg Val Gly Thr Thr Thr Asn Gly Val Asn
 35 40 45
 Gln Gln Ala Gln Gly Thr Phe Gln Gly Ser Thr Phe Pro Gly Arg Asp
 50 55 60
 Ile Ala Trp Val Ala Thr Asn Ala Asn Trp Thr Pro Arg Pro Leu Val
 65 70 75 80
 Asn Gly Tyr Gly Arg Gly Asp Val Thr Val Ala Gly Ser Thr Ala Ser
 85 90 95
 Val Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His
 100 105 110
 Cys Gly Thr Ile Gln Gln Leu Asn Thr Ser Val Thr Tyr Pro Glu Gly
 115 120 125
 Thr Ile Ser Gly Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp
 130 135 140
 Ser Gly Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser
 145 150 155 160
 Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro
 165 170 175
 Ile Asn Pro Leu Leu Gln Ala Tyr Gly Leu Thr Leu Val Thr Ser Gly
 180 185 190
 Gly Gly Thr Pro Thr Asp Pro Pro Thr Thr Pro Pro Thr Asp Ser Pro
 195 200 205
 Gly Gly Thr Trp Ala Val Gly Thr Ala Tyr Ala Ala Gly Ala Thr Val
 210 215 220
 Thr Tyr Gly Gly Ala Thr Tyr Arg Cys Leu Gln Ala His Thr Ala Gln
 225 230 235 240
 Pro Gly Trp Thr Pro Ala Asp Val Pro Ala Leu Trp Gln Arg Val
 245 250 255

<210> 640
 <211> 185
 <212> PRT
 <213> Streptogrisin B

<400> 640

Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg Cys Ser Leu

<210> 642
 <211> 188
 <212> PRT
 <213> Streptogrisin D

<400> 642

Ile	Ala	Gly	Gly	Asp	Ala	Ile	Trp	Gly	Ser	Gly	Ser	Arg	Cys	Ser	Leu
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Gly	Phe	Asn	Val	Val	Lys	Gly	Gly	Glu	Pro	Tyr	Phe	Leu	Thr	Ala	Gly
			20					25					30		
His	Cys	Thr	Glu	Ser	Val	Thr	Ser	Trp	Ser	Asp	Thr	Gln	Gly	Gly	Ser
		35					40					45			
Glu	Ile	Gly	Ala	Asn	Glu	Gly	Ser	Ser	Phe	Pro	Glu	Asn	Asp	Tyr	Gly
	50					55					60				
Leu	Val	Lys	Tyr	Thr	Ser	Asp	Thr	Ala	His	Pro	Ser	Glu	Val	Asn	Leu
65					70					75					80
Tyr	Asp	Gly	Ser	Thr	Gln	Ala	Ile	Thr	Gln	Ala	Gly	Asp	Ala	Thr	Val
				85					90					95	
Gly	Gln	Ala	Val	Thr	Arg	Ser	Gly	Ser	Thr	Thr	Gln	Val	His	Asp	Gly

				100											
								105						110	
Glu	Val	Thr	Ala	Leu	Asp	Ala	Thr	Val	Asn	Tyr	Gly	Asn	Gly	Asp	Ile
			115					120					125		
Val	Asn	Gly	Leu	Ile	Gln	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser
			130				135					140			
Gly	Gly	Ala	Leu	Phe	Ala	Gly	Asp	Thr	Ala	Leu	Gly	Leu	Thr	Ser	Gly
145					150					155					160
Gly	Ser	Gly	Asp	Cys	Ser	Ser	Gly	Gly	Thr	Thr	Phe	Phe	Gln	Pro	Val
				165					170					175	
Pro	Glu	Ala	Leu	Ala	Ala	Tyr	Gly	Ala	Glu	Ile	Gly				
			180					185							

<210> 643
 <211> 198
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

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 <222> (9)..(10)
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 <222> (12)..(12)
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<223> Xaa can be any naturally occurring amino acid

<400> 643

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Leu Gly Phe Asn Val Xaa Xaa Gly Xaa Xaa Xaa Tyr Phe Leu Thr Ala
          20          25          30
Gly His Cys Thr Xaa Xaa Gly Thr Thr Trp Xaa Xaa Xaa Xaa Xaa
          35          40          45
Xaa Xaa Xaa Ile Gly Thr Xaa Xaa Gly Ser Ser Phe Pro Xaa Asn Asp
          50          55          60
Tyr Gly Ile Val Arg Tyr Thr Ala Xaa Xaa Xaa Xaa Xaa Xaa Val
65          70          75          80
Asn Xaa Tyr Xaa Gly Xaa Xaa Gln Xaa Ile Thr Xaa Ala Gly Xaa Ala
          85          90          95
Xaa Val Gly Xaa Ala Val Xaa Arg Ser Gly Ser Thr Thr Gly Xaa His
          100         105         110
Xaa Gly Ser Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Xaa Gly
          115         120         125
Xaa Ile Val Xaa Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly
          130         135         140
Asp Ser Gly Gly Ser Leu Phe Ala Gly Ser Xaa Ala Leu Gly Leu Thr
145         150         155         160
Ser Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln
          165         170         175
Pro Val Xaa Glu Ala Leu Ser Ala Tyr Gly Leu Thr Val Ile Xaa Xaa
          180         185         190
Xaa Xaa Xaa Xaa Xaa
          195
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<210> 644

<211> 513

<212> PRT

<213> Thermus aquaticus

<400> 644

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1          5          10          15
Gly Gly Cys Gln Met Ala Ser Arg Ser Asp Pro Thr Pro Thr Leu Ala
          20          25          30
Glu Ala Phe Trp Pro Lys Glu Ala Pro Val Tyr Gly Leu Asp Asp Pro
          35          40          45
Glu Ala Ile Pro Gly Arg Tyr Ile Val Val Phe Lys Lys Gly Lys Gly
          50          55          60
Gln Ser Leu Leu Gln Gly Gly Ile Thr Thr Leu Gln Ala Arg Leu Ala
65          70          75          80
Pro Gln Gly Val Val Val Thr Gln Ala Tyr Thr Gly Ala Leu Gln Gly
          85          90          95
Phe Ala Ala Glu Met Ala Pro Gln Ala Leu Glu Ala Phe Arg Gln Ser
          100         105         110
Pro Asp Val Glu Phe Ile Glu Ala Asp Lys Val Val Arg Ala Trp Ala
          115         120         125
Thr Gln Ser Pro Ala Pro Trp Gly Leu Asp Arg Ile Asp Gln Arg Asp
          130         135         140
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Leu	Pro	Leu	Ser	Asn	Ser	Tyr	Thr	Tyr	Thr	Ala	Thr	Gly	Arg	Gly	Val
145					150					155					160
Asn	Val	Tyr	Val	Ile	Asp	Thr	Gly	Ile	Arg	Thr	Thr	His	Arg	Glu	Phe
				165					170					175	
Gly	Gly	Arg	Ala	Arg	Val	Gly	Tyr	Asp	Ala	Leu	Gly	Gly	Asn	Gly	Gln
			180					185					190		
Asp	Cys	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Thr	Ile	Gly	Gly	Val
	195						200					205			
Thr	Tyr	Gly	Val	Ala	Lys	Ala	Val	Asn	Leu	Tyr	Ala	Val	Arg	Val	Leu
	210					215					220				
Asp	Cys	Asn	Gly	Ser	Gly	Ser	Thr	Ser	Gly	Val	Ile	Ala	Gly	Val	Asp
225				230						235					240
Trp	Val	Thr	Arg	Asn	His	Arg	Arg	Pro	Ala	Val	Ala	Asn	Met	Ser	Leu
				245					250					255	
Gly	Gly	Gly	Val	Ser	Thr	Ala	Leu	Asp	Asn	Ala	Val	Lys	Asn	Ser	Ile
			260					265					270		
Ala	Ala	Gly	Val	Val	Tyr	Ala	Val	Ala	Ala	Gly	Asn	Asp	Asn	Ala	Asn
		275					280					285			
Ala	Cys	Asn	Tyr	Ser	Pro	Ala	Arg	Val	Ala	Glu	Ala	Leu	Thr	Val	Gly
	290					295					300				
Ala	Thr	Thr	Ser	Ser	Asp	Ala	Arg	Ala	Ser	Phe	Ser	Asn	Tyr	Gly	Ser
305					310					315					320
Cys	Val	Asp	Leu	Phe	Ala	Pro	Gly	Ala	Ser	Ile	Pro	Ser	Ala	Trp	Tyr
				325					330					335	
Thr	Ser	Asp	Thr	Ala	Thr	Gln	Thr	Leu	Asn	Gly	Thr	Ser	Met	Ala	Thr
			340					345					350		
Pro	His	Val	Ala	Gly	Val	Ala	Ala	Leu	Tyr	Leu	Glu	Gln	Asn	Pro	Ser
		355					360					365			
Ala	Thr	Pro	Ala	Ser	Val	Ala	Ser	Ala	Ile	Leu	Asn	Gly	Ala	Thr	Thr
		370				375					380				
Gly	Arg	Leu	Ser	Gly	Ile	Gly	Ser	Gly	Ser	Pro	Asn	Arg	Leu	Leu	Tyr
385					390					395					400
Ser	Leu	Leu	Ser	Ser	Gly	Ser	Gly	Ser	Thr	Ala	Pro	Cys	Thr	Ser	Cys
				405				410						415	
Ser	Tyr	Tyr	Thr	Gly	Ser	Leu	Ser	Gly	Pro	Gly	Asp	Tyr	Asn	Phe	Gln
			420					425					430		
Pro	Asn	Gly	Thr	Tyr	Tyr	Tyr	Ser	Pro	Ala	Gly	Thr	His	Arg	Ala	Trp
		435					440					445			
Leu	Arg	Gly	Pro	Ala	Gly	Thr	Asp	Phe	Asp	Leu	Tyr	Leu	Trp	Arg	Trp
	450					455					460				
Asp	Gly	Ser	Arg	Trp	Leu	Thr	Val	Gly	Ser	Ser	Thr	Gly	Pro	Thr	Ser
465					470					475					480
Glu	Glu	Ser	Leu	Ser	Tyr	Ser	Gly	Thr	Ala	Gly	Tyr	Tyr	Leu	Trp	Arg
				485					490					495	
Ile	Tyr	Ala	Tyr	Ser	Gly	Ser	Gly	Met	Tyr	Glu	Phe	Trp	Leu	Gln	Arg
			500					505					510		

Pro

<210> 645

<211> 495

<212> PRT

<213> Cellulomonas strain 69B4

<400> 645

Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala

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Ala	Thr	Leu	Leu	Ala	Gly	Gly	Met	Ala	Ala	Gln	Ala	Asn	Glu	Pro	Ala
		20						25					30		
Pro	Pro	Gly	Ser	Ala	Ser	Ala	Pro	Pro	Arg	Leu	Ala	Glu	Lys	Leu	Asp
		35					40					45			
Pro	Asp	Leu	Leu	Glu	Ala	Met	Glu	Arg	Asp	Leu	Gly	Leu	Asp	Ala	Glu
		50				55					60				
Glu	Ala	Ala	Ala	Thr	Leu	Ala	Phe	Gln	His	Asp	Ala	Ala	Glu	Thr	Gly
65				70					75					80	
Glu	Ala	Leu	Ala	Glu	Glu	Leu	Asp	Glu	Asp	Phe	Ala	Gly	Thr	Trp	Val
		85						90					95		
Glu	Asp	Asp	Val	Leu	Tyr	Val	Ala	Thr	Thr	Asp	Glu	Asp	Ala	Val	Glu
		100						105					110		
Glu	Val	Glu	Gly	Glu	Gly	Ala	Thr	Ala	Val	Thr	Val	Glu	His	Ser	Leu
		115					120					125			
Ala	Asp	Leu	Glu	Ala	Trp	Lys	Thr	Val	Leu	Asp	Ala	Ala	Leu	Glu	Gly
		130				135					140				
His	Asp	Asp	Val	Pro	Thr	Trp	Tyr	Val	Asp	Val	Pro	Thr	Asn	Ser	Val
145				150					155					160	
Val	Val	Ala	Val	Lys	Ala	Gly	Ala	Gln	Asp	Val	Ala	Ala	Gly	Leu	Val
		165						170					175		
Glu	Gly	Ala	Asp	Val	Pro	Ser	Asp	Ala	Val	Thr	Phe	Val	Glu	Thr	Asp
		180					185					190			
Glu	Thr	Pro	Arg	Thr	Met	Phe	Asp	Val	Ile	Gly	Gly	Asn	Ala	Tyr	Thr
		195					200					205			
Ile	Gly	Gly	Arg	Ser	Arg	Cys	Ser	Ile	Gly	Phe	Ala	Val	Asn	Gly	Gly
		210				215					220				
Phe	Ile	Thr	Ala	Gly	His	Cys	Gly	Arg	Thr	Gly	Ala	Thr	Thr	Ala	Asn
225				230					235					240	
Pro	Thr	Gly	Thr	Phe	Ala	Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala
		245						250					255		
Phe	Val	Arg	Thr	Gly	Ala	Gly	Val	Asn	Leu	Leu	Ala	Gln	Val	Asn	Asn
		260					265					270			
Tyr	Ser	Gly	Gly	Arg	Val	Gln	Val	Ala	Gly	His	Thr	Ala	Ala	Pro	Val
		275					280					285			
Gly	Ser	Ala	Val	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys	Gly
		290				295					300				
Thr	Ile	Thr	Ala	Leu	Asn	Ser	Ser	Val	Thr	Tyr	Pro	Glu	Gly	Thr	Val
305				310					315					320	
Arg	Gly	Leu	Ile	Arg	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly
		325						330					335		
Gly	Ser	Leu	Leu	Ala	Gly	Asn	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly
		340					345					350			
Ser	Gly	Asn	Cys	Arg	Thr	Gly	Gly	Thr	Thr	Phe	Phe	Gln	Pro	Val	Asn
		355				360						365			
Pro	Ile	Leu	Gln	Ala	Tyr	Gly	Leu	Arg	Met	Ile	Thr	Thr	Asp	Ser	Gly
		370				375					380				
Ser	Ser	Pro	Ala	Pro	Ala	Pro	Thr	Ser	Cys	Thr	Gly	Tyr	Ala	Arg	Thr
385				390					395					400	
Phe	Thr	Gly	Thr	Leu	Ala	Ala	Gly	Arg	Ala	Ala	Ala	Gln	Pro	Asn	Gly
		405					410					415			
Ser	Tyr	Val	Gln	Val	Asn	Arg	Ser	Gly	Thr	His	Ser	Val	Cys	Leu	Asn
		420					425					430			
Gly	Pro	Ser	Gly	Ala	Asp	Phe	Asp	Leu	Tyr	Val	Gln	Arg	Trp	Asn	Gly
		435				440					445				
Ser	Ser	Trp	Val	Thr	Val	Ala	Gln	Ser	Thr	Ser	Pro	Gly	Ser	Asn	Glu
450						455					460				

Thr	Ile	Thr	Tyr	Arg	Gly	Asn	Ala	Gly	Tyr	Tyr	Arg	Tyr	Val	Val	Asn
465					470				475						480
Ala	Ala	Ser	Gly	Ser	Gly	Ala	Tyr	Thr	Met	Gly	Leu	Thr	Leu	Pro	
				485				490						495	

<210> 646
 <211> 510
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<220>
 <221> VARIANT
 <222> (3)..(509)
 <223> Xaa can be any naturally occurring amino acid

<400> 646

Met	Ala	Xaa	Xaa	Ala	Xaa	Xaa	Leu	Leu	Ala	Gly	Xaa	Xaa	Xaa	Ala	Xaa
1				5					10					15	
Xaa	Xaa	Asp	Pro	Xaa	Pro	Xaa	Xaa	Ala	Xaa	Ala	Xaa	Xaa	Pro	Lys	Xaa
			20					25					30		
Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Glu	Ala	Ile	Xaa	Xaa	Xaa	Xaa
			35				40					45			
Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Gln	Xaa	Xaa
	50					55			60						
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa
65						70			75					80	
Xaa	Xaa	Phe	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85					90					95	
Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Glu	Xaa	Xaa	Xaa	Xaa
			100					105					110		
Ala	Xaa	Xaa	Val	Xaa	Xaa	Ala	Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			115				120						125		
Xaa	Leu	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Tyr
	130					135					140				
Xaa	Xaa	Xaa	Xaa	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Val	Xaa	Xaa	Ile	Xaa	Xaa
145				150						155				160	
Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Val	Xaa
				165					170					175	
Xaa	Asp	Ala	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			180					185					190		
Xaa	Met	Xaa	Xaa	Xaa	Ile	Gly	Gly	Xaa	Xaa	Tyr	Xaa	Ile	Ala	Xaa	Xaa
	195					200						205			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Ala
	210					215				220					
Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Xaa
225					230					235				240	
Xaa	Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Ala	Gly	Xaa	Xaa	Xaa	Xaa	Ala
				245					250					255	
Xaa	Asp	Xaa	Ala	Xaa	Xaa	Xaa	Ser	Xaa	Ala	Ala	Xaa	Xaa	Xaa	Xaa	Xaa
			260					265					270		
Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Ala	Asn	Xaa	Xaa	Asn	Tyr	Ser	Xaa	Ala
	275						280					285			
Arg	Val	Xaa	Xaa	Ala	Xaa	Xaa	Xaa	Ala	Ala	Xaa	Xaa	Xaa	Ser	Xaa	Xaa

290		295		300
Xaa Xaa Ser Xaa Ser Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa				
305		310		315
Xaa Ala Xaa Xaa Xaa Ser Xaa Xaa Tyr Xaa Xaa Xaa Thr Xaa Xaa Xaa				
		325		330
Xaa Ile Xaa Xaa Thr Xaa Xaa Ala Xaa Pro Xaa Xaa Ala Gly Xaa Ala				
		340		345
Xaa Leu Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Thr Xaa Ala Xaa Xaa Ala				
		355		360
Xaa Xaa Xaa Xaa Xaa Gly Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa				
		370		375
Xaa Xaa Ala Xaa Xaa Xaa Xaa Leu Xaa Ser Xaa Xaa Ser Xaa Gly Ser				
385		390		395
Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Cys Ser Xaa Tyr Xaa Xaa Ser Xaa				
		405		410
Ser Gly Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Gln Pro Asn Gly Ser				
		420		425
Tyr Xaa Xaa Xaa Xaa Xaa Ala Gly Thr His Xaa Xaa Xaa Leu Xaa Gly				
		435		440
Pro Ala Gly Xaa Asp Phe Asp Leu Tyr Leu Xaa Arg Trp Xaa Gly Ser				
		450		455
Xaa Trp Leu Thr Val Ala Xaa Ser Thr Xaa Pro Xaa Ser Xaa Glu Ser				
465		470		475
Ile Ser Tyr Xaa Gly Xaa Ala Gly Tyr Tyr Xaa Trp Xaa Ile Xaa Ala				
		485		490
Xaa Ser Gly Ser Gly Xaa Tyr Xaa Xaa Xaa Leu Xaa Xaa Pro				
		500		505
				510

<210> 647

<211> 190

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<220>

<221> VARIANT

<222> (6)..(188)

<223> Xaa can be any naturally occurring amino acid

<400> 647

Asp Val Ile Gly Gly Xaa Xaa Tyr Xaa Ile Xaa Xaa Xaa Xaa Arg Xaa				
1		5		10
Xaa Xaa Xaa Xaa Cys Ser Ile Gly Phe Ala Val Xaa Gly Gly Phe Val				
		20		25
Thr Ala Gly His Cys Gly Arg Xaa Gly Ala Xaa Xaa Xaa Xaa Xaa Xaa				
		35		40
Thr Ser Xaa Pro Xaa Gly Thr Phe Xaa Gly Ser Ser Phe Pro Gly Asn				
		50		55
Asp Tyr Ala Trp Val Gln Val Ala Ser Gly Asn Thr Pro Val Gly Ala				
65		70		75
Val Asn Asn Tyr Ser Gly Gly Thr Val Xaa Val Ala Gly Ser Thr Xaa				
		85		90
Ala Ala Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp				
		100		105
				110

Arg	Cys	Gly	Thr	Ile	Xaa	Ala	Tyr	Asn	Ala	Ser	Val	Xaa	Tyr	Ala	Glu
		115					120					125			
Gly	Thr	Val	Ser	Gly	Leu	Ile	Arg	Thr	Asn	Val	Cys	Ala	Glu	Pro	Gly
		130				135					140				
Asp	Ser	Gly	Gly	Ser	Leu	Leu	Ala	Gly	Asn	Gln	Ala	Gln	Gly	Val	Thr
145					150					155					160
Ser	Gly	Gly	Ser	Gly	Asn	Cys	Xaa	Xaa	Gly	Gly	Thr	Thr	Tyr	Phe	Gln
				165					170					175	
Pro	Val	Asn	Xaa	Xaa	Leu	Xaa	Xaa	Tyr	Gly	Leu	Xaa	Leu	Val		
			180					185					190		

<210> 648
 <211> 368
 <212> PRT
 <213> Thermobifida fusca

<400> 648

Met	Asn	His	Ser	Ser	Arg	Arg	Thr	Thr	Ser	Leu	Leu	Phe	Thr	Ala	Ala
1				5					10					15	
Leu	Ala	Ala	Thr	Ala	Leu	Val	Ala	Ala	Thr	Thr	Pro	Ala	Ser	Ala	Gln
			20					25					30		
Glu	Leu	Ala	Leu	Lys	Arg	Asp	Leu	Gly	Leu	Ser	Asp	Ala	Glu	Val	Ala
		35					40					45			
Glu	Leu	Arg	Ala	Ala	Glu	Ala	Glu	Ala	Val	Glu	Leu	Glu	Glu	Glu	Leu
	50					55				60					
Arg	Asp	Ser	Leu	Gly	Ser	Asp	Phe	Gly	Gly	Val	Tyr	Leu	Asp	Ala	Asp
65					70					75					80
Thr	Thr	Glu	Ile	Thr	Val	Ala	Val	Thr	Asp	Pro	Ala	Ala	Val	Ser	Arg
				85					90					95	
Val	Asp	Ala	Asp	Asp	Val	Thr	Val	Asp	Val	Val	Asp	Phe	Gly	Glu	Thr
			100					105					110		
Ala	Leu	Asn	Asp	Phe	Val	Ala	Ser	Leu	Asn	Ala	Ile	Ala	Asp	Thr	Ala
		115					120					125			
Asp	Pro	Lys	Val	Thr	Gly	Trp	Tyr	Thr	Asp	Leu	Glu	Ser	Asp	Ala	Val
	130					135					140				
Val	Ile	Thr	Thr	Leu	Arg	Gly	Gly	Thr	Pro	Ala	Ala	Glu	Glu	Leu	Ala
145					150					155					160
Glu	Arg	Ala	Gly	Leu	Asp	Glu	Arg	Ala	Val	Arg	Ile	Val	Glu	Glu	Asp
				165					170					175	
Glu	Glu	Pro	Gln	Ser	Leu	Ala	Ala	Ile	Ile	Gly	Gly	Asn	Pro	Tyr	Tyr
			180					185					190		
Phe	Gly	Asn	Tyr	Arg	Cys	Ser	Ile	Gly	Phe	Ser	Val	Arg	Gln	Gly	Ser
		195					200					205			
Gln	Thr	Gly	Phe	Ala	Thr	Ala	Gly	His	Cys	Gly	Ser	Thr	Gly	Thr	Arg
	210					215					220				
Val	Ser	Ser	Pro	Ser	Gly	Thr	Val	Ala	Gly	Ser	Tyr	Phe	Pro	Gly	Arg
225					230					235					240
Asp	Met	Gly	Trp	Val	Arg	Ile	Thr	Ser	Ala	Asp	Thr	Val	Thr	Pro	Leu
				245					250					255	
Val	Asn	Arg	Tyr	Asn	Gly	Gly	Thr	Val	Thr	Val	Thr	Gly	Ser	Gln	Glu
			260				265						270		
Ala	Ala	Thr	Gly	Ser	Ser	Val	Cys	Arg	Ser	Gly	Ala	Thr	Thr	Gly	Trp
		275					280					285			
Arg	Cys	Gly	Thr	Ile	Gln	Ser	Lys	Asn	Gln	Thr	Val	Arg	Tyr	Ala	Glu
	290					295					300				
Gly	Thr	Val	Thr	Gly	Leu	Thr	Arg	Thr	Thr	Ala	Cys	Ala	Glu	Gly	Gly

305		310		315		320									
Asp	Ser	Gly	Gly	Pro	Trp	Leu	Thr	Gly	Ser	Gln	Ala	Gln	Gly	Val	Thr
		325						330						335	
Ser	Gly	Gly	Thr	Gly	Asp	Cys	Arg	Ser	Gly	Gly	Ile	Thr	Phe	Phe	Gln
		340						345					350		
Pro	Ile	Asn	Pro	Leu	Leu	Ser	Tyr	Phe	Gly	Leu	Gln	Leu	Val	Thr	Gly
		355					360						365		

<210> 649
 <211> 382
 <212> PRT
 <213> Streptomyces spp.

<400> 649

Met	Arg	His	Thr	Gly	Arg	Asn	Ala	Ile	Gly	Ala	Ala	Ile	Ala	Ala	Ser
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Ala	Leu	Ala	Phe	Ala	Leu	Val	Pro	Ser	Gln	Ala	Ala	Ala	Asn	Asp	Thr
			20					25					30		
Leu	Thr	Glu	Arg	Ala	Glu	Ala	Ala	Val	Ala	Asp	Leu	Pro	Ala	Gly	Val
		35					40					45			
Leu	Asp	Ala	Met	Glu	Arg	Asp	Leu	Gly	Leu	Ser	Glu	Gln	Glu	Ala	Gly
	50					55					60				
Leu	Lys	Leu	Val	Ala	Glu	His	Asp	Ala	Ala	Leu	Leu	Gly	Glu	Thr	Leu
65					70					75					80
Ser	Ala	Asp	Leu	Asp	Ala	Phe	Ala	Gly	Ser	Trp	Leu	Ala	Glu	Gly	Thr
			85					90					95		
Glu	Leu	Val	Val	Ala	Thr	Thr	Ser	Glu	Ala	Glu	Ala	Ala	Glu	Ile	Thr
			100					105					110		
Glu	Ala	Gly	Ala	Thr	Ala	Glu	Val	Val	Asp	His	Thr	Leu	Ala	Glu	Leu
		115					120					125			
Asp	Ser	Val	Lys	Asp	Ala	Leu	Asp	Thr	Ala	Ala	Glu	Ser	Tyr	Asp	Thr
	130					135					140				
Thr	Asp	Ala	Pro	Val	Trp	Tyr	Val	Asp	Val	Thr	Thr	Asn	Gly	Val	Val
145					150					155					160
Leu	Leu	Thr	Ser	Asp	Val	Thr	Glu	Ala	Glu	Gly	Phe	Val	Glu	Ala	Ala
				165					170					175	
Gly	Val	Asn	Ala	Ala	Ala	Val	Asp	Ile	Gln	Thr	Ser	Asp	Glu	Gln	Pro
			180					185					190		
Gln	Ala	Phe	Tyr	Asp	Leu	Val	Gly	Gly	Asp	Ala	Tyr	Tyr	Met	Gly	Gly
		195					200					205			
Gly	Arg	Cys	Ser	Val	Gly	Phe	Ser	Val	Thr	Gln	Gly	Ser	Thr	Pro	Gly
	210					215					220				
Phe	Ala	Thr	Ala	Gly	His	Cys	Gly	Thr	Val	Gly	Thr	Ser	Thr	Thr	Gly
225					230					235					240
Tyr	Asn	Gln	Ala	Ala	Gln	Gly	Thr	Phe	Glu	Glu	Ser	Ser	Phe	Pro	Gly
			245						250					255	
Asp	Asp	Met	Ala	Trp	Val	Ser	Val	Asn	Ser	Asp	Trp	Asn	Thr	Thr	Pro
			260					265					270		
Thr	Val	Asn	Glu	Gly	Glu	Val	Thr	Val	Ser	Gly	Ser	Thr	Glu	Ala	Ala
		275					280						285		
Val	Gly	Ala	Ser	Ile	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys
	290					295					300				
Gly	Thr	Ile	Gln	Gln	His	Asn	Thr	Ser	Val	Thr	Tyr	Pro	Glu	Gly	Thr
305					310					315					320
Ile	Thr	Gly	Val	Thr	Arg	Thr	Ser	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser
				325					330					335	

Gly Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly
340 345 350
Gly Ser Gly Asn Cys Thr Ser Gly Gly Thr Thr Tyr His Gln Pro Ile
355 360 365
Asn Pro Leu Leu Ser Ala Tyr Gly Leu Asp Leu Val Thr Gly
370 375 380

<210> 650
<211> 388
<212> PRT
<213> Streptomyces spp.

<400> 650

Met Arg Leu Lys Gly Arg Thr Val Ala Ile Gly Ser Ala Leu Ala Ala
1 5 10 15
Ser Ala Leu Ala Leu Ser Leu Val Pro Ala Asn Ala Ser Ser Glu Leu
20 25 30
Pro Ser Ala Glu Thr Ala Lys Ala Asp Ala Leu Val Glu Gln Leu Pro
35 40 45
Ala Gly Met Val Asp Ala Met Glu Arg Asp Leu Gly Val Pro Ala Ala
50 55 60
Glu Val Gly Asn Gln Leu Val Ala Glu His Glu Ala Ala Val Leu Glu
65 70 75 80
Glu Ser Leu Ser Glu Asp Leu Ser Gly Tyr Ala Gly Ser Trp Ile Val
85 90 95
Glu Gly Thr Ser Glu His Val Val Ala Thr Thr Asp Arg Ala Glu Ala
100 105 110
Ala Glu Ile Thr Ala Ala Gly Ala Thr Ala Thr Val Val Glu His Ser
115 120 125
Leu Ala Glu Leu Glu Ala Val Lys Asp Ile Leu Asp Glu Ala Ala Thr
130 135 140
Ala Asn Pro Glu Asp Ala Ala Pro Val Trp Tyr Val Asp Val Thr Thr
145 150 155 160
Asn Glu Val Val Val Leu Ala Ser Asp Val Pro Ala Ala Glu Ala Phe
165 170 175
Val Ala Ala Ser Gly Ala Asp Ala Ser Thr Val Arg Val Glu Arg Ser
180 185 190
Asp Glu Ser Pro Gln Pro Phe Tyr Asp Leu Val Gly Gly Asp Ala Tyr
195 200 205
Tyr Ile Gly Asn Gly Arg Cys Ser Ile Gly Phe Ser Val Arg Gln Gly
210 215 220
Ser Thr Pro Gly Phe Val Thr Ala Gly His Cys Gly Ser Val Gly Asn
225 230 235 240
Ala Thr Thr Gly Phe Asn Arg Val Ser Gln Gly Thr Phe Arg Gly Ser
245 250 255
Trp Phe Pro Gly Arg Asp Met Ala Trp Val Ala Val Asn Ser Asn Trp
260 265 270
Thr Pro Thr Ser Leu Val Arg Asn Ser Gly Ser Gly Val Arg Val Thr
275 280 285
Gly Ser Thr Gln Ala Thr Val Gly Ser Ser Ile Cys Arg Ser Gly Ser
290 295 300
Thr Thr Gly Trp Arg Cys Gly Thr Ile Gln Gln His Asn Thr Ser Val
305 310 315 320
Thr Tyr Pro Gln Gly Thr Ile Thr Gly Val Thr Arg Thr Ser Ala Cys
325 330 335
Ala Gln Pro Gly Asp Ser Gly Gly Ser Phe Ile Ser Gly Thr Gln Ala

			340					345					350				
Gln	Gly	Val	Thr	Ser	Gly	Gly	Ser	Gly	Asn	Cys	Ser	Ile	Gly	Gly	Thr		
		355					360					365					
Thr	Phe	His	Gln	Pro	Val	Asn	Pro	Ile	Leu	Ser	Gln	Tyr	Gly	Leu	Thr		
	370					375					380						
Leu	Val	Arg	Ser														
385																	

<210> 651
 <211> 458
 <212> PRT
 <213> Streptomyces lividans
 <400> 651

Met	Val	Gly	Arg	His	Ala	Ala	Arg	Ser	Arg	Arg	Ala	Ala	Leu	Thr	Ala		
1				5					10					15			
Leu	Gly	Ala	Leu	Val	Leu	Thr	Ala	Leu	Pro	Ser	Ala	Ala	Ser	Ala	Ala		
			20					25					30				
Pro	Pro	Pro	Val	Pro	Gly	Pro	Arg	Pro	Ala	Val	Ala	Arg	Thr	Pro	Asp		
		35					40					45					
Ala	Ala	Thr	Ala	Pro	Ala	Arg	Met	Leu	Ser	Ala	Met	Glu	Arg	Asp	Leu		
	50					55					60						
Arg	Leu	Ala	Pro	Gly	Gln	Ala	Ala	Ala	Arg	Pro	Val	Asn	Glu	Ala	Glu		
65					70				75						80		
Ala	Gly	Thr	Arg	Ala	Gly	Met	Leu	Arg	Asn	Thr	Leu	Gly	Asp	Arg	Phe		
			85						90					95			
Ala	Gly	Ala	Trp	Val	Ser	Gly	Ala	Thr	Ser	Ala	Glu	Leu	Thr	Val	Ala		
			100					105					110				
Thr	Thr	Asp	Ala	Ala	Asp	Thr	Ala	Ala	Ile	Glu	Ala	Gln	Gly	Ala	Lys		
		115					120					125					
Ala	Ala	Val	Val	Gly	Arg	Asn	Leu	Ala	Glu	Leu	Arg	Ala	Val	Lys	Glu		
	130					135					140						
Lys	Leu	Asp	Ala	Ala	Ala	Val	Arg	Thr	Arg	Thr	Arg	Gln	Thr	Pro	Val		
145					150					155					160		
Trp	Tyr	Val	Asp	Val	Lys	Thr	Asn	Arg	Val	Thr	Val	Gln	Ala	Thr	Gly		
			165						170					175			
Ala	Ser	Ala	Ala	Ala	Phe	Val	Glu	Ala	Ala	Gly	Val	Pro	Ala	Ala			
			180				185					190					
Asp	Val	Gly	Val	Arg	Val	Ser	Pro	Asp	Gln	Pro	Arg	Val	Leu	Glu	Asp		
	195						200					205					
Leu	Val	Gly	Gly	Asp	Ala	Tyr	Tyr	Ile	Asp	Asp	Gln	Ala	Arg	Cys	Ser		
	210					215					220						
Ile	Gly	Phe	Ser	Val	Thr	Lys	Asp	Asp	Gln	Glu	Gly	Phe	Ala	Thr	Ala		
225					230				235						240		
Gly	His	Cys	Gly	Asp	Pro	Gly	Ala	Thr	Thr	Thr	Gly	Tyr	Asn	Glu	Ala		
			245						250					255			
Asp	Gln	Gly	Thr	Phe	Gln	Ala	Ser	Thr	Phe	Pro	Gly	Lys	Asp	Met	Ala		
			260						265					270			
Trp	Val	Gly	Val	Asn	Ser	Asp	Trp	Thr	Ala	Thr	Pro	Asp	Val	Lys	Ala		
		275					280					285					
Glu	Gly	Gly	Glu	Lys	Ile	Gln	Leu	Ala	Gly	Ser	Val	Glu	Ala	Leu	Val		
	290					295					300						
Gly	Ala	Ser	Val	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys	Gly		
305					310					315					320		
Thr	Ile	Gln	Gln	His	Asp	Thr	Ser	Val	Thr	Tyr	Pro	Glu	Gly	Thr	Val		
				325					330					335			

Asp	Gly	Leu	Thr	Gly	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly		
			340					345					350				
Gly	Pro	Phe	Val	Ser	Gly	Val	Gln	Ala	Gln	Gly	Thr	Thr	Ser	Gly	Gly		
		355					360					365					
Ser	Gly	Asp	Cys	Thr	Asn	Gly	Gly	Thr	Thr	Phe	Tyr	Gln	Pro	Val	Asn		
	370					375					380						
Pro	Leu	Leu	Ser	Asp	Phe	Gly	Leu	Thr	Leu	Lys	Thr	Thr	Ser	Ala	Ala		
385					390					395					400		
Thr	Gln	Thr	Pro	Ala	Pro	Gln	Asp	Asn	Ala	Ala	Ala	Asp	Ala	Trp	Thr		
			405						410					415			
Ala	Gly	Arg	Val	Tyr	Glu	Val	Gly	Thr	Thr	Val	Ser	Tyr	Asp	Gly	Val		
		420					425						430				
Arg	Tyr	Arg	Cys	Leu	Gln	Ser	His	Gln	Ala	Gln	Gly	Val	Gly	Ser	Pro		
	435						440					445					
Ala	Ser	Val	Pro	Ala	Leu	Trp	Gln	Arg	Val								
	450					455											

<210> 652

<211> 458

<212> PRT

<213> Streptomyces coelicolor A3(2)

<400> 652

Met	Val	Gly	Arg	His	Ala	Ala	Arg	Ser	Arg	Arg	Ala	Ala	Leu	Thr	Ala		
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Leu	Gly	Ala	Leu	Val	Leu	Thr	Ala	Leu	Pro	Ser	Ala	Ala	Ser	Ala	Ala		
		20						25					30				
Pro	Pro	Pro	Val	Pro	Gly	Pro	Arg	Pro	Ala	Val	Ala	Arg	Thr	Pro	Asp		
		35					40					45					
Ala	Ala	Thr	Ala	Pro	Ala	Arg	Met	Leu	Ser	Ala	Met	Glu	Arg	Asp	Leu		
	50					55					60						
Arg	Leu	Ala	Pro	Gly	Gln	Ala	Ala	Ala	Arg	Leu	Val	Asn	Glu	Ala	Glu		
65				70					75					80			
Ala	Gly	Thr	Arg	Ala	Gly	Met	Leu	Arg	Asn	Thr	Leu	Gly	Asp	Arg	Phe		
			85					90					95				
Ala	Gly	Ala	Trp	Val	Ser	Gly	Ala	Thr	Ser	Ala	Glu	Leu	Thr	Val	Ala		
		100						105					110				
Thr	Thr	Asp	Ala	Ala	Asp	Thr	Ala	Ala	Ile	Glu	Ala	Gln	Gly	Ala	Lys		
		115					120					125					
Ala	Ala	Val	Val	Gly	Arg	Asn	Leu	Ala	Glu	Leu	Arg	Ala	Val	Lys	Glu		
	130					135					140						
Lys	Leu	Asp	Ala	Ala	Ala	Val	Arg	Thr	Arg	Thr	Arg	Gln	Thr	Pro	Val		
145			150						155					160			
Trp	Tyr	Val	Asp	Val	Lys	Thr	Asn	Arg	Val	Thr	Val	Gln	Ala	Thr	Gly		
		165						170						175			
Ala	Ser	Ala	Ala	Ala	Ala	Phe	Val	Glu	Ala	Ala	Gly	Val	Pro	Ala	Ala		
		180						185					190				
Asp	Val	Gly	Val	Arg	Val	Ser	Pro	Asp	Gln	Pro	Arg	Val	Leu	Glu	Asp		
	195					200					205						
Leu	Val	Gly	Gly	Asp	Ala	Tyr	Tyr	Ile	Asp	Asp	Gln	Ala	Arg	Cys	Ser		
	210					215					220						
Ile	Gly	Phe	Ser	Val	Thr	Lys	Asp	Asp	Gln	Glu	Gly	Phe	Ala	Thr	Ala		
225				230					235					240			
Gly	His	Cys	Gly	Asp	Pro	Gly	Ala	Thr	Thr	Gly	Tyr	Asn	Glu	Ala			
		245						250					255				
Asp	Gln	Gly	Thr	Phe	Gln	Ala	Ser	Thr	Phe	Pro	Gly	Lys	Asp	Met	Ala		

			260					265				270					
Trp	Val	Gly	Val	Asn	Ser	Asp	Trp	Thr	Ala	Thr	Pro	Asp	Val	Lys	Ala		
		275						280				285					
Glu	Gly	Gly	Glu	Lys	Ile	Gln	Leu	Ala	Gly	Ser	Val	Glu	Ala	Leu	Val		
		290					295					300					
Gly	Ala	Ser	Val	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys	Gly		
305					310						315				320		
Thr	Ile	Gln	Gln	His	Asp	Thr	Ser	Val	Thr	Tyr	Pro	Glu	Gly	Thr	Val		
				325						330				335			
Asp	Gly	Leu	Thr	Glu	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly		
			340					345					350				
Gly	Pro	Phe	Val	Ser	Gly	Val	Gln	Ala	Gln	Gly	Thr	Thr	Ser	Gly	Gly		
		355					360						365				
Ser	Gly	Asp	Cys	Thr	Asn	Gly	Gly	Thr	Thr	Phe	Tyr	Gln	Pro	Val	Asn		
	370					375					380						
Pro	Leu	Leu	Ser	Asp	Phe	Gly	Leu	Thr	Leu	Lys	Thr	Thr	Ser	Ala	Ala		
385					390					395					400		
Thr	Gln	Thr	Pro	Ala	Pro	Gln	Asp	Asn	Ala	Ala	Ala	Asp	Ala	Trp	Thr		
				405					410					415			
Ala	Gly	Arg	Val	Tyr	Glu	Val	Gly	Thr	Thr	Val	Ser	Tyr	Asp	Gly	Val		
			420					425					430				
Arg	Tyr	Arg	Cys	Leu	Gln	Ser	His	Gln	Ala	Gln	Gly	Val	Gly	Ser	Pro		
		435					440					445					
Ala	Ser	Val	Pro	Ala	Leu	Trp	Gln	Arg	Val								
	450					455											

<210> 653
 <211> 456
 <212> PRT
 <213> Streptomyces avermitilis MA-4680

<400> 653

Met Val His Arg His Val Gly Ala Gly Cys Ala Gly Leu Ser Val Leu

1				5				10					15				
Ala	Thr	Leu	Val	Leu	Thr	Gly	Leu	Pro	Ala	Ala	Ala	Ala	Ile	Glu	Pro		
			20					25					30				
Pro	Gly	Pro	Ala	Pro	Ala	Pro	Ser	Ala	Val	Gln	Pro	Leu	Gly	Ala	Gly		
		35					40					45					
Asn	Pro	Ser	Thr	Ala	Val	Leu	Gly	Ala	Leu	Gln	Arg	Asp	Leu	His	Leu		
	50					55				60							
Thr	Asp	Thr	Gln	Ala	Lys	Thr	Arg	Leu	Val	Asn	Glu	Met	Glu	Ala	Gly		
65					70					75				80			
Thr	Arg	Ala	Gly	Arg	Leu	Gln	Asn	Ala	Leu	Gly	Lys	His	Phe	Ala	Gly		
			85					90					95				
Ala	Trp	Val	His	Gly	Ala	Ala	Ser	Ala	Asp	Leu	Thr	Val	Ala	Thr	Thr		
		100						105					110				
His	Ala	Thr	Asp	Ile	Pro	Ala	Ile	Thr	Ala	Gly	Gly	Ala	Thr	Ala	Val		
		115					120					125					
Val	Val	Lys	Thr	Gly	Leu	Asp	Asp	Leu	Lys	Gly	Ala	Lys	Lys	Lys	Leu		
	130					135				140							
Asp	Ser	Ala	Val	Ala	His	Gly	Gly	Thr	Ala	Val	Asn	Thr	Pro	Val	Arg		
145					150					155					160		
Tyr	Val	Asp	Val	Arg	Thr	Asn	Arg	Val	Thr	Leu	Gln	Ala	Arg	Ser	Arg		
			165					170					175				

Ala Ala Ala Asp Ala Leu Ile Ala Ala Ala Gly Val Asp Ser Gly Leu
 180 185 190
 Val Asp Val Lys Val Ser Glu Asp Arg Pro Arg Ala Leu Phe Asp Ile
 195 200 205
 Arg Gly Gly Asp Ala Tyr Tyr Ile Asp Asn Thr Ala Arg Cys Ser Val
 210 215 220
 Gly Phe Ser Val Thr Lys Gly Asn Gln Gln Gly Phe Ala Thr Ala Gly
 225 230 235 240
 His Cys Gly Arg Ala Gly Ala Pro Thr Ala Gly Phe Asn Glu Val Ala
 245 250 255
 Gln Gly Thr Val Gln Ala Ser Val Phe Pro Gly His Asp Met Ala Trp
 260 265 270
 Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val Ala Gly Ala
 275 280 285
 Ala Gly Gln Asn Val Ser Ile Ala Gly Ser Val Gln Ala Ile Val Gly
 290 295 300
 Ala Ala Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr
 305 310 315 320
 Val Glu Glu His Asp Thr Ser Val Thr Tyr Glu Glu Gly Thr Val Asp
 325 330 335
 Gly Leu Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly
 340 345 350
 Ser Phe Val Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser
 355 360 365
 Gly Asp Cys Thr Arg Gly Gly Thr Thr Tyr Tyr Gln Pro Val Asn Pro
 370 375 380
 Ile Leu Ser Thr Tyr Gly Leu Thr Leu Lys Thr Ser Thr Ala Pro Thr
 385 390 395 400
 Asp Thr Pro Ser Asp Pro Val Asp Gln Ser Gly Val Trp Ala Ala Gly
 405 410 415
 Arg Val Tyr Glu Val Gly Ala Gln Val Thr Tyr Ala Gly Val Thr Tyr
 420 425 430
 Gln Cys Leu Gln Ser His Gln Ala Gln Gly Val Trp Gln Pro Ala Ala
 435 440 445
 Thr Pro Ala Leu Trp Gln Arg Leu
 450 455

<210> 654

<211> 458

<212> PRT

<213> Streptomyces lividans

<400> 654

Met Pro His Arg His Arg His His Arg Ala Val Gly Ala Ala Val Ala
 1 5 10 15
 Ala Thr Ala Ala Leu Leu Val Ala Gly Leu Ser Gly Ser Ala Ser Ala
 20 25 30
 Gly Thr Ala Pro Ala Gly Ser Ala Pro Thr Ala Ala Glu Thr Leu Arg
 35 40 45
 Thr Asp Ala Ala Pro Pro Ala Leu Leu Lys Ala Met Gln Arg Asp Leu
 50 55 60
 Gly Ile Asp Arg Arg Gln Ala Glu Arg Arg Leu Val Asn Glu Ala Glu
 65 70 75 80
 Ala Gly Ala Thr Ala Gly Arg Leu Arg Ala Ala Leu Gly Gly Asp Phe
 85 90 95
 Ala Gly Ala Trp Val Arg Gly Ala Glu Ser Gly Thr Leu Thr Val Ala

			100					105				110			
Thr	Thr	Asp	Ala	Gly	Asp	Val	Ala	Ala	Val	Glu	Ala	Arg	Gly	Ala	Glu
		115					120					125			
Ala	Lys	Val	Val	Arg	His	Ser	Leu	Ala	Asp	Leu	Asp	Ala	Ala	Lys	Ala
	130					135					140				
Arg	Leu	Asp	Thr	Ala	Ala	Ala	Gly	Leu	Asn	Thr	Ala	Asp	Ala	Pro	Val
145				150					155					160	
Trp	Tyr	Val	Asp	Thr	Arg	Thr	Asn	Thr	Val	Val	Val	Glu	Ala	Ile	Arg
		165						170						175	
Pro	Ala	Ala	Ala	Arg	Ser	Leu	Leu	Thr	Ala	Ala	Gly	Val	Asp	Gly	Ser
	180						185						190		
Leu	Ala	His	Val	Lys	Asn	Arg	Thr	Glu	Arg	Pro	Arg	Thr	Phe	Tyr	Asp
	195						200					205			
Leu	Arg	Gly	Gly	Glu	Ala	Tyr	Tyr	Ile	Asn	Asn	Ser	Ser	Arg	Cys	Ser
	210					215					220				
Ile	Gly	Phe	Pro	Ile	Thr	Lys	Gly	Thr	Gln	Gln	Gly	Phe	Ala	Thr	Ala
225				230					235					240	
Gly	His	Cys	Asp	Arg	Ala	Gly	Ser	Ser	Thr	Thr	Gly	Ala	Asn	Arg	Val
		245						250						255	
Ala	Gln	Gly	Thr	Phe	Gln	Gly	Ser	Ile	Phe	Pro	Gly	Arg	Asp	Met	Ala
	260							265					270		
Trp	Val	Ala	Thr	Asn	Ser	Ser	Trp	Thr	Ala	Thr	Pro	Tyr	Val	Leu	Gly
	275						280					285			
Ala	Gly	Gly	Gln	Asn	Val	Gln	Val	Thr	Gly	Ser	Thr	Ala	Ser	Pro	Val
	290					295					300				
Gly	Ala	Ser	Val	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys	Gly
305				310					315					320	
Thr	Val	Thr	Gln	Leu	Asn	Thr	Ser	Val	Thr	Tyr	Gln	Glu	Gly	Thr	Ile
		325						330						335	
Ser	Pro	Val	Thr	Arg	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly
	340						345						350		
Gly	Ser	Phe	Ile	Ser	Gly	Ser	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly
	355					360						365			
Ser	Gly	Asp	Cys	Arg	Thr	Gly	Gly	Gly	Thr	Phe	Phe	Gln	Pro	Ile	Asn
	370					375					380				
Ala	Leu	Leu	Gln	Asn	Tyr	Gly	Leu	Thr	Leu	Lys	Thr	Thr	Gly	Gly	Asp
385				390					395					400	
Asp	Gly	Gly	Gly	Asp	Asp	Gly	Gly	Glu	Glu	Pro	Gly	Gly	Thr	Trp	Ala
		405						410						415	
Ala	Gly	Thr	Val	Tyr	Gln	Pro	Gly	Asp	Thr	Val	Thr	Tyr	Gly	Gly	Ala
	420						425						430		
Thr	Phe	Arg	Cys	Leu	Gln	Gly	His	Gln	Ala	Tyr	Ala	Gly	Trp	Glu	Pro
	435					440						445			
Pro	Asn	Val	Pro	Ala	Leu	Trp	Gln	Arg	Val						
	450					455									

<210> 655

<211> 463

<212> PRT

<213> Streptomyces coelicolor A3(2)

<400> 655

Met	Pro	His	Arg	His	Arg	His	His	Arg	Ala	Val	Gly	Ala	Ala	Val	Ala
1				5				10						15	
Ala	Thr	Ala	Ala	Leu	Leu	Val	Ala	Gly	Leu	Ser	Gly	Ser	Ala	Ser	Ala
		20						25						30	

<212> PRT

<213> Streptomyces griseus

<400> 656

Met	Glu	Arg	Thr	Thr	Leu	Arg	Arg	Arg	Ala	Leu	Val	Ala	Gly	Thr	Ala
1				5					10					15	
Thr	Val	Ala	Val	Gly	Ala	Leu	Ala	Leu	Ala	Gly	Leu	Thr	Gly	Val	Ala
			20					25					30		
Ser	Ala	Asp	Pro	Ala	Ala	Thr	Ala	Ala	Pro	Pro	Val	Ser	Ala	Asp	Ser
		35					40					45			
Leu	Ser	Pro	Gly	Met	Leu	Ala	Ala	Leu	Glu	Arg	Asp	Leu	Gly	Leu	Asp
	50				55						60				
Glu	Asp	Ala	Ala	Arg	Ser	Arg	Ile	Ala	Asn	Glu	Tyr	Arg	Ala	Ala	Ala
65					70					75				80	
Val	Ala	Ala	Gly	Leu	Glu	Lys	Ser	Leu	Gly	Ala	Arg	Tyr	Ala	Gly	Ala
				85					90					95	
Arg	Val	Ser	Gly	Ala	Lys	Ala	Thr	Leu	Thr	Val	Ala	Thr	Thr	Asp	Ala
			100					105					110		
Ser	Glu	Ala	Ala	Arg	Ile	Thr	Glu	Ala	Gly	Ala	Arg	Ala	Glu	Val	Val
		115					120					125			
Gly	His	Ser	Leu	Asp	Arg	Phe	Glu	Gly	Val	Lys	Lys	Ser	Leu	Asp	Lys
	130					135					140				
Ala	Ala	Leu	Asp	Lys	Ala	Pro	Lys	Asn	Val	Pro	Val	Trp	Tyr	Val	Asp
145					150					155				160	
Val	Ala	Ala	Asn	Arg	Val	Val	Val	Asn	Ala	Ala	Ser	Pro	Ala	Ala	Gly
				165					170					175	
Gln	Ala	Phe	Leu	Lys	Val	Ala	Gly	Val	Asp	Arg	Gly	Leu	Val	Thr	Val
			180					185					190		
Ala	Arg	Ser	Ala	Glu	Gln	Pro	Arg	Ala	Leu	Ala	Asp	Ile	Arg	Gly	Gly
		195					200					205			
Asp	Ala	Tyr	Tyr	Met	Asn	Gly	Ser	Gly	Arg	Cys	Ser	Val	Gly	Phe	Ser
	210					215					220				
Val	Thr	Arg	Gly	Thr	Gln	Asn	Gly	Phe	Ala	Thr	Ala	Gly	His	Cys	Gly
225					230					235				240	
Arg	Val	Gly	Thr	Thr	Asn	Gly	Val	Asn	Gln	Gln	Ala	Gln	Gly	Thr	
				245					250				255		
Phe	Gln	Gly	Ser	Thr	Phe	Pro	Gly	Arg	Asp	Ile	Ala	Trp	Val	Ala	Thr
			260					265					270		
Asn	Ala	Asn	Trp	Thr	Pro	Arg	Pro	Leu	Val	Asn	Gly	Tyr	Gly	Arg	Gly
		275					280					285			
Asp	Val	Thr	Val	Ala	Gly	Ser	Thr	Ala	Ser	Val	Val	Gly	Ala	Ser	Val
	290					295					300				
Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys	Gly	Thr	Ile	Gln	Gln
305					310					315				320	
Leu	Asn	Thr	Ser	Val	Thr	Tyr	Pro	Glu	Gly	Thr	Ile	Ser	Gly	Val	Thr
				325					330					335	
Arg	Thr	Ser	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	Gly	Ser	Tyr	Ile
			340					345					350		
Ser	Gly	Ser	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly	Ser	Gly	Asn	Cys
		355					360					365			
Ser	Ser	Gly	Gly	Thr	Thr	Tyr	Phe	Gln	Pro	Ile	Asn	Pro	Leu	Leu	Gln
	370					375					380				
Ala	Tyr	Gly	Leu	Thr	Leu	Val	Thr	Ser	Gly	Gly	Gly	Thr	Pro	Thr	Asp
385					390					395				400	
Pro	Pro	Thr	Thr	Pro	Pro	Thr	Asp	Ser	Pro	Gly	Gly	Thr	Trp	Ala	Val
				405					410					415	

Gly Thr Ala Tyr Ala Ala Gly Ala Thr Val Thr Tyr Gly Gly Ala Thr
420 425 430
Tyr Arg Cys Leu Gln Ala His Thr Ala Gln Pro Gly Trp Thr Pro Ala
435 440 445
Asp Val Pro Ala Leu Trp Gln Arg Val
450 455